

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 07:42:35 ; Search time 28 Seconds
(without alignments)
1209.582 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDYQVSSPIVDINYTTSEPC.....ERASSVYTRSTGEQISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	2 A43113	chemokine (C-C) re
2	1359	73.8	360	2 JC2443	chemokine (C-C) re
3	1219	66.2	374	2 I38450	chemokine (C-C) re
4	1059	57.5	355	2 A45177	chemokine (C-C) re
5	1011.5	54.9	355	2 I49339	macrophage inflam
6	1003.5	54.5	359	2 I49341	MIP-1 alpha recept
7	936.5	50.9	355	2 G02436	chemokine (C-C) re
8	914	49.6	360	2 A57160	chemokine (C-C) re
9	901	48.9	360	2 JC4587	chemokine (C-C) re
10	832	45.2	383	2 S55594	G protein-coupled
11	802.5	43.6	356	2 I49340	MIP-1 alpha recept
12	751.5	40.8	355	2 JC5067	G protein-coupled
13	717	38.9	354	2 I58186	probable G protein
14	675.5	36.7	355	2 JC4304	orphan G protein-c
15	670	36.4	344	2 JC5942	chemokine receptor
16	562	30.5	378	2 B55735	lymphocyte-specifi
17	560	30.4	378	2 A55735	G protein-coupled
18	554	30.1	369	2 JC5068	G protein-coupled
19	548	29.8	378	2 A45680	G protein-coupled
20	542	29.4	333	2 I65989	G protein-coupled
21	520	28.2	360	2 A53611	interleukin-8 rece
22	516.5	28.1	359	2 A48921	interleukin-8 rece
23	514	27.9	355	2 JQ1231	interleukin-8 rece
24	513.5	27.9	358	2 A53752	interleukin-8 rece
25	505.5	27.5	350	2 A39445	interleukin-8 rece
26	505.5	27.5	367	2 JE0349	interferon-inducib
27	504.5	27.4	350	2 JN0621	G protein-coupled
28	501	27.2	352	2 G00048	fusin (LESTRA) - c
29	501	27.2	352	2 A45747	neuropeptide Y/pep

30 491.5 26.7 353 2 S28787 neuropeptide Y/pep
31 489.5 26.6 356 2 J42096 interleukin-8 rece
32 473.5 25.7 359 2 JC2134 angiotensin II rec
33 472.5 25.7 359 2 A42856 angiotensin II rec
34 470 25.5 359 2 I51372 angiotensin II rec
35 468.5 25.4 359 2 JH0621 angiotensin II rec
36 468 25.4 374 2 S44268 G protein-coupled
37 467.5 25.4 359 2 S44425 angiotensin II rec
38 467.5 25.4 359 2 JCL1194 angiotensin II rec
39 465.5 25.3 359 2 S15403 angiotensin II rec
40 463.5 25.2 359 2 JQ1516 angiotensin II rec
41 460.5 25.0 359 2 JCL1104 angiotensin II rec
42 459.5 25.0 359 2 A48857 angiotensin II rec
43 457 24.8 327 2 S56162 MCR15 protein - h
44 457 24.8 372 2 S26667 G protein-coupled
45 449 24.4 374 2 S32785 G protein-coupled

ALIGNMENTS

RESULT 1

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000

C;Accession: A43113; S71808; A58834; A58832; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine recept

A;Reference number: A43113; MUID:96241590; PMID:8639485

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:G1262810; PIDN:CAAG2796.1; PID:G1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosa

M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; P

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles

A;Reference number: S71808; MUID:96345670; PMID:8751444

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184,'IKDSHLAGAPAAACHGILLGNPKNSASVSK' <SAM3>

A;Cross-references: GB:X9393; NID:G1524062; PIDN:CAAG7767.1; PID:G1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a deg

nd may have had a selective advantage by conferring resistance to Yersinia plague infec

R;Combadiere, C.; Anuja, S.K.; Tiffany, H.L.; Murphy, P.W.

J. Leukoc. Biol. 60, 147-152, 1996

A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine re

A;Reference number: A58832; MUID:96295970; PMID:8699119

A;Accession: A58832

A;Molecule type: mRNA

A;Residues: 1-352 <COM1>

A;Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409

A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

R;Combadiere, C.

submitted to the EMBL Data Library, May 1996

A;Reference number: H01541

A;Accession: G02653

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-89,'L',91-352 <COM2>

A;Cross-references: EMBL:U57840

R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.

J. Biol. Chem. 271, 17161-17166, 1996

A;Title: Molecular cloning and functional characterization of a novel human CC chemokin

A;Reference number: A58833; MUID:96291862; PMID:8663314

C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM2>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 49.6%; Score 914; DB 2; Length 360;
Best Local Similarity 49.6%; Pred. No. 2e-67;
Matches 175; Conservative 68; Mismatches 100; Indels 10; Gaps 6;

QY 2 DYQVSSPIYDINVTSE----PCOKINVKQIAARLLPPLYSLVPIFGVGNMLVILILIN 57
DB 8 DTLDESIS-NYLYESIPKCTKEGKAFGELFPLPLYSLVFVFGLLGNSVVVLIFK 66
QY 58 CKRLKSMTDIYLLMAISDLFFLLTPVFWAHYLAQWDFGNMTCOLLTGLYFGFRSGIF 117
DB 67 YKRLRSMTDVLLMAISDLFFVSLFPGWGYAADQWVFGGLCKMISWMLVGFYSGIF 126
QY 118 FIILLTIDRYLAVHAVFALKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYT 177
DB 127 FVLMISIDRYLAVHAVFSLRARTLTGVTSLATWSVAVFASLPGLFSTCYTERNHTY 186
QY 178 CSHHPYSQYQWKNFOTLKIVILGLVPLVAVMVCYSGILKTLRCNKKRRAVRLI 237
DB 187 CKTKYSLNS-TTWKVLSSLEINILGLVPLGIMLFCYSMIIRTLQHCNKK-NKAVMI 244
QY 238 FTIMIVFLFWAFNIVLLANTQEPFGLNCSNRLDOAMQVTELTGTHCCINPIIY 297
DB 245 FAVVLFLGFWTFNIVLFETLVEVLQDCTFERYLDYAIQATETLGFTHCCINPIY 304
QY 298 AFVGEKFRNLLVFFQKHAKRF--CKCCSIFQOEAPERASSVYTRSTGEQE 348
DB 305 FFLGKFRKYLQLF-KTCRGLFVLCQYGLLIQIYSADTPSSSYTQSTVDHDL 356

RESULT 9
JC4587
Chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g116
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: Glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 48.9%; Score 901; DB 2; Length 360;

Best Local Similarity 49.6%; Pred. No. 2.3e-66;
Matches 170; Conservative 69; Mismatches 98; Indels 6; Gaps 4;

QY 9 IYDINY--TSPPCKINVKQIAARLLPPLYSLVPIFGVGNMLVILILINCKRLKSM 65
DB 15 VINSYFYESMPKPCKEGKAFGEVFLPPLYSLVFLGFGNSVVVLVFLFKYKRLKSM 74
QY 66 DIYLLMAISDLFFLLTPVFWAHYLAQWDFGNMTCOLLTGLYFGIFGFIIFILLTID 125
DB 75 DVYLLMAISDLFFVLSLPPWGYAADQWVFGGLCKIVSMVMVLVGYSGIFFLMLSID 134
QY 126 RYLAVHAVFALKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSSHPYS 185
DB 135 RYLAVHAVFSLKARTLTGVTSLATWSVAVFASLPGLFSTCYTERNHTYCKTQSVN 194
QY 186 QYQWKNFOTLKIVILGLVPLVAVMVCYSGILKTLRCNKKRRAVRLITIMIVYF 245
DB 195 S-TTWKVLSSLEINILGLVPLGIMLFCYSMIIRTLQHCNKK-NRAVRMIFGVVFL 252
QY 246 LFWAPYNIYLLNTQEPFGLNCSNRLDOAMQVTELTGTHCCINPIIYAFVGEKFR 305
DB 253 GFWTPNVVLFETLVEVLQDCTLERYLDYAIQATETLGFTHCCINPIYFLGKFR 312
QY 306 NYLLVFFQKHAKR-FCKCCSIFQOEAPERASSVYTRSTGEQE 347
DB 313 KYITQLFTRCGRPLVLCCKHCDFLQVYSADMSSSYTQSTVDHD 355

RESULT 10
S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S55594

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

C;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g69517

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 45.2%; Score 832; DB 2; Length 383;

Best Local Similarity 47.4%; Pred. No. 1.1e-60;

Matches 157; Conservative 65; Mismatches 101; Indels 8; Gaps 3;

QY 11 DINYTSEPCOKINVKQIAARLLPPLYSLVPIFGVGNMLVILILINCKRLKSM 70
DB 53 DVDEESAPCYSDTTRLAAQVVPALYLVFLGGLGNILWIIIVRYMKIRLTMWLL 112
QY 71 NLAISDLFLLTVPFWAHYLA--QWDFGNMTCOLLTGLYFGIFGFIIFILLTIDRYL 128
DB 113 NLAISDLFLLTVPFWHYGMVHWDTFGISLCKLRGVCYMSLYSQVFCILLTVDRL 172
QY 129 AVHAVFALKARTVTGVTSTVITWVAVFASLPGLIIFTRSQEGLHYTCSSHPYSQY 188
DB 173 AVVAVTALRFRFTVTCGIVTCVCTWPLAGLLSLPEFFHGHQDNGRVQCDYPPMSTN 232
QY 189 FKNFOTLKIVILGLVPLVAVMVCYSGILKTLRCNKKRRAVRLITIMIVYFLFW 248
DB 233 VMRAHVAKVIIMLSLPLIMAVCYVIRLLR-RPSKKYKAIKRLVIMVAVYFVW 291
QY 249 APNIVLLANTQEPFGLNCSNRLDOAMQVTELTGTHCCINPIIYAFVGEKFRN 308
DB 292 TPNIVLLSTTHATLLNQALSSMLDMLITKIVATHCCINPIIYAFVGEKFRHL 351
QY 309 LVFFQKHAKRFCKCCSIFQ-----QEAPER 334
DB 352 YHFFHTYVAILCKYIPFLSGDGEKGPTR 382

RESULT 11

I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49340
R;Geo, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881549
C;Superfamily: vertebrate rhodopsin

Query Match 43.6%; Score 802.5; DB 2; Length 356;
Best Local Similarity 45.0%; Pred. No. 2.6e-58;
Matches 159; Conservative 69; Mismatches 118; Indels 7; Gaps 4;

```
QY 5 VSSPIYDI----NYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
DB 6 VTSPSYNTAKNDFMGFLCFSINVRAGITVPTPLYSLVIFITGVGHVLVVLVLIQHR 65

QY 61 LKSMTDIYLNLAISDLFFLLTVPFWAHY-LAAQWDFGNMTCOLLGLYPIGFSGIFFI 119
DB 66 LRNWTSIYFNLAISDLVFLSTLPFWVDYIMKGDWIFGNACKFVSGFYLYGLYDMFEI 125

QY 120 ILTIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCS 179
DB 126 TLLTIDRYLAVHVAHFALRARTVTFGIISIIITWVLAALVSIPLCYVFKSQMEFTYHTR 185

QY 180 SHEPYSQYQWKNFOTLKIIVILGLVPLVMWVLCYSGILKTLARCNEKKRHRVRLIFT 239
DB 186 AILPRKSLIRFLRQALTMNIGLIDPLLAIIICYTRIINVLNR-RPNKKAKMRLIFV 244

QY 240 IMTVYFLWAPYINVLNLTFOFFGLNCGSSNRLDQAMQVETLGMTGCCINPIIYAF 299
DB 245 ITLLFFLLAPYLAAFVSAFEDVILFTPSCLRSQOVDLSLMIETALAYTHCCVNPVIYF 304

QY 300 VSKFERNYLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGBOEISVGL 352
DB 305 VGRFRKRYLWQLFRRHITAILPQWLPLPSLSDRAQASALPSTVETIETSDAL 356
```

RESULT 12

JC5067
G protein-coupled receptor CRK-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C:Accession: JC5067; G02387
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G proteins.
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067
A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: UNIPROT:P51685; NID:g1668735; PIDN:CAB02142.1; PID:g1668735
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996

A;Reference number: H01154

A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBR12; TER1; CRK-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 40.8%; Score 751.5; DB 2; Length 355;
Best Local Similarity 41.4%; Pred. No. 3.8e-54;
Matches 149; Conservative 66; Mismatches 124; Indels 21; Gaps 6;

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QY 1 MDYQSSPIYDI-NYY----TSEPQKINVKQIAARLLPPLYSLVIFGFVGNMLVILIL 55
DB 1 MDYTLDSLTVTVDYYPDIFSSPCDAELIQTNKLLAVFYCLLFVFLGNSLVILVL 60

QY 56 INCKRLKSMTDIYLNLAISDLFFLLTVPFWAHYLAQWDFGNMTCOLLGLYFGFFSG 115
DB 61 VVCKLRSITDYLNLALSDLLFVSPFQYLLDQWVFGVMCKVSGFYIIGFYIS 120

QY 116 IFFIILLTIDRYLAVHVAHFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLH 175
DB 121 MFFITLMSVDRLVAVHVAHFALVIRMGTTTLCIAVWLTAIWTATPLLVFYQVASEDGV 180

QY 176 YTCSSHPYSQYQWKNFOTLKIIVILGLVPLVMWVLCYSGILKTLRCNEKKRHRV 235
DB 181 LQCYIS-FYNQOTLKWKIFTNFMNIGLLIPIFTIFMFCYIKILHQLKRCQNHKT-KAIR 238

QY 236 LIFTIMIVYFLWAPYINVLNLTFOFFGLNCGSSNRLDQAMQVETLGMTGCCINPI 295
DB 239 LVLIVVIASLLFWPVPNVVLFITLSHSMILDCSSISQQLTYATHVTEIISFTHCCVNPV 298

QY 296 IYAFVGEKERNYLVFFQKHIAKFCCKCSIFQ-----QOEAPERASSVYTRSTGQEI 348
DB 299 IYAFVGEKFKHLSEIFQK-----SCSQIFNVLGRQMPRESCCKSSCQHQSSRSSV 351
```

RESULT 13

I58186
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and identified as a member of the chemokine receptor family.
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g43411
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 38.9%; Score 717; DB 2; Length 354;
Best Local Similarity 40.9%; Pred. No. 2.5e-51;
Matches 148; Conservative 59; Mismatches 125; Indels 30; Gaps 6;

QY 6 SSPDIYDNY----TSEPQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKRL 61

```
Db 4 SFPELDLENFSDSAEACVGLDVAFGTIFLSIFSLVFTFGVGNLLVVALTNSRKS 63
QY 62 KSMTDIYLLNLAISDLFELLTPFWAHYLAOWDFGNTMQLLGLYFIFGFSIGIFRIL 121
Db 64 KSITDIYLLNLAISDLFVATLPFWTHYLSHEGLHNAKCLTATFFIFGFGIFITV 123
QY 122 LTIDRYLAHVHAPALKARTVTFGVTSVITWVAVFASLPGIIFTRSQEGLHYTCS 181
Db 124 ISIDRYLAIVLAANSMNRITVQHGVTISLGVWAAAILVASPQFMFTKRDN----ECLGD 179
QY 182 FPIYQYQFNKPFQTLKIVILGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIM 241
Db 180 YPEVLQIWPVLENSVNIILGVLPLIMSFYRIVRTILFSCNKKKA-RAIRLILLV 238
QY 242 IVVFLFWAPYNIULLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFVG 301
Db 239 VVFLFWTPYNIIVFLFTLKYFNFPSCGMKDRLWALSVTETVAFPSHCCLNPIIYAFAG 298
QY 302 EKFRNYLLVFFQKHIAKRFCKCCSIF-----QOEAPERASSVYTRSTGRQEI 348
Db 299 EKFRNYL-----RHL-----YKCLAVLCGRPVHAGFSTESQRQDSILSLTHYTSRGE 350
QY 349 SV 350
Db 351 SL 352
```

RESULT 14

```
JC4304
Orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:G665580; PIDN:AAA91783.1; PID:G665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
C;Genetics:
A;Gene: V28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>
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Query Match 36.7%; Score 675.5; DB 2; Length 355;
Best Local Similarity 43.2%; Pred. No. 6.4e-48;
Matches 130; Conservative 55; Mismatches 111; Indels 5; Gaps 3;
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QY 17 SEPCQKINVKQIAARLLPPLYSLVFIYFGVGNMLVILLINCKRLKSMTDIYLLNLAISD 76
Db 18 AEACYIGDIVVFGTFLSIFYSVIPAIGLVGNLLVWVAFALTNKSKPSVTDIYLLNLAISD 77
QY 77 LFPELLTPFWAHYLAOWDFGNTMQLLGLYFIFGFSIGIFRILTIIDRYLAHVHAPVA 136
Db 78 LLFVATLPFWTHYLINELKGLHNAKCTTATFFIFGFSIGIFRITVISIDRYLAIVLAANS 137
QY 137 LKARTVTFGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSHPFYQYQFNKPFQTL 196
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Db 138 MNRRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKEN----ECLGDYDEVLQEIWVPLRNV 193
QY 197 KIVILGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIMIVYVFLFWAPYNIULL 256
Db 194 ETFLGFLPPELLMSYCYFRIIQTLSCKNHKA-KAUKULLLVVIVVFFLFWTPYNNWIF 252
QY 257 LNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHI 316
Db 253 LETLKLKYDFPPSCDMRDLRLALSVTETVAFPSHCCLNPLIYAFAGEKFRNYLHYLKGCL 312
QY 317 A 317
Db 313 A 313
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RESULT 15

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JC5942
chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC5942
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <FAN>
A;Cross-references: UNIPROT:O00421; GB:U97123; NID:G2897070; PIDN:AAC39595.1; PID:G2897
C;Superfamily: vertebrate rhodopsin
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Query Match 36.4%; Score 670; DB 2; Length 344;
Best Local Similarity 40.9%; Pred. No. 1.7e-47;
Matches 137; Conservative 64; Mismatches 108; Indels 26; Gaps 7;
QY 17 SEPCQKINVKQIAARLLPPLYSLVFIYFGVGNMLVILLINCKRLKSMTDIYLLNLAISD 76
Db 25 AEQCDKYDAQALSQALVPSLCSAVFVIGVLDNLVLLVKYKGLKRVENIYLLNLAISN 84
QY 77 LFPELLTPFWAHYLAOWDFGNTMQLLGLYFIFGFSIGIFRILTIIDRYLAHVH-AVF 135
Db 85 LCPELLTPFWAH-----AGGDPMKILIGLYFVGLYSETFFNCLLTQVQRYLFLHKGNF 138
QY 136 ALKARTVTFGVTSVITWVAVFASLPGIIFTRSQEGLHYTCS-SHPFY--SQYQFNK 192
Db 139 FSARRVPVCGIITSVLAWVTAILATLPEYVYVKPQMEDQKYKCAFSTRPPLPADETFWKH 198
QY 193 FQTLKIVILGLVLPILVMVICYSGLKTLRCNEKKRRAVRLIFTIMIVYVFLFWAPYN 252
Db 199 FULTKNVISVLVLPFLFIFLYVQMKTL---RFRQRYSLFKLVFAIMVWVFLMWAPYN 255
QY 253 IVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFVGEKFRNYLLVFF 312
Db 256 IAPFLSTFKHEFSLSDCKSYNLDKSVHTKLITATTHCCINPLLYAFLDGTFSKYL---- 311
QY 313 QKHIARFKCKCSIFQOEAPERASSVYTRSTGEQE 347
Db 312 -----CRCFHL-RSNTPLQPRGQSAQTSREE 337
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Search completed: October 3, 2005, 07:48:34
Job time : 29 secs

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GenCore version 5.1.6
Copyright: (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 06:53:54 ; Search time 98 Seconds
(without alignments)
1839.305 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDYQVSSPIYDINYTTSEPC.....ERASSVYTRSTGRGEISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	1	CKR5 HUMAN
2	1830	99.4	352	1	CKR5 PANPA
3	1830	99.4	352	1	CKR5 PANTR
4	1825	99.1	352	1	CKR5 PONPA
5	1825	99.1	352	1	CKR5 PONPY
6	1825	99.1	352	2	Q71T22
7	1820	98.9	352	1	CKR5 GORGO
8	1820	98.9	352	1	CKR5 HYLVS
9	1820	98.9	352	2	Q71T20
10	1820	98.9	352	2	Q71T21
11	1818	98.8	352	2	O18771
12	1818	98.8	352	2	O18772
13	1817	98.7	352	2	Q9XS99
14	1816	98.6	352	1	CKR5 SEMEN
15	1816	98.6	352	1	CKR5 TRAPH
16	1816	98.6	352	2	Q71T26
17	1816	98.6	352	2	Q9TV50
18	1813	98.5	352	1	CKR5 HYLML
19	1812	98.4	352	2	Q9SNC7
20	1811	98.4	352	1	CKR5 LOPAT
21	1811	98.4	352	1	CKR5 PAPAN
22	1811	98.4	352	1	CKR5 PAPHA
23	1811	98.4	352	2	Q9SNC8
24	1811	98.4	352	2	Q9SNC8
25	1811	98.4	352	2	Q71U18
26	1810	98.3	352	1	CKR5 PYGBI
27	1810	98.3	352	1	CKR5 PYGNE
28	1809	98.3	352	1	CKR5 HYLL
29	1808	98.2	352	1	CKR5 MACFA
30	1808	98.2	352	1	CKR5 MACMU
31	1808	98.2	352	1	CKR5 MACNE

32	1808	98.2	352	2	O97962
33	1808	98.2	352	2	Q71T27
34	1808	98.2	352	2	Q71T28
35	1808	98.2	352	2	Q71T29
36	1808	98.2	352	2	Q7J34
37	1807	98.2	352	2	O9SNC1
38	1807	98.2	352	2	Q9XT14
39	1806	98.1	352	2	Q9SNC3
40	1806	98.1	352	2	Q9SNC6
41	1804	98.0	352	2	Q9XT13
42	1803	97.9	352	2	O18770
43	1803	97.9	352	2	Q9TSK1
44	1803	97.9	352	2	Q9TV49
45	1802	97.9	352	2	O97975

ALIGNMENTS

RESULT 1

ID	CKR5_HUMAN	STANDARD	PRT	352 AA
AC	P51681	O14693; O14696; O14697; O14698; O14699; O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707; O14708; O15538; Q9UPA4;		
DT	01-OCT-1996	(Rel. 34, Created)		
DT	25-OCT-2004	(Rel. 45, Last sequence update)		
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS) (HIV-1 fusion coreceptor) (CHEMR13) (CD195 antigen).			
GN	Name=CCRS5; Synonyms=CMKBR5;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96241590; PubMed=8639485; DOI=10.1021/bi952950g;			
RA	Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;			
RT	"Molecular cloning and functional expression of a new human CC-chemokine receptor gene."			
RL	Biochemistry 35:3362-3367(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96291862; PubMed=8663314; DOI=10.1074/jbc.271.29.17161;			
RA	Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;			
RT	"Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."			
RL	J. Biol. Chem. 271:17161-17166(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96295970; PubMed=8699119;			
RA	Combariere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;			
RT	"Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and RANTES."			
RL	J. Leukoc. Biol. 60:147-152(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastie M., Kaplan N., Grisco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98001387; PubMed=9343222;			
RA	Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;			
RT	"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human			

RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Rutherford C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RL to D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201; DOI=10.1074/jbc.272.49.30662;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
RA Magierowska M., Barre-Sinoussi F., Isenhardt H., Theodorou I.,
RL Debre P.;
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260017; PubMed=8649511; DOI=10.1038/381661a0;
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
RL di Marzio P., Martin S., Sutton R.E., Hill C.M., Davis C.B.,
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
RT "Identification of a major co-receptor for primary isolates of HIV-
RT 1.";
RL Nature 381:661-666(1996).
RN [11]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE=96260018; PubMed=8649512; DOI=10.1038/381667a0;
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
RL Nagashima K.A., Cavanan C., Maddon P.J., Koup R.A., Moore J.P.,
RA Paxton W.A.;
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor CC-
RT CR-5.";
RL Nature 381:667-673(1996).
RN [12]
RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882; DOI=10.1016/S0092-8674(00)80577-2;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RL Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry.";
RL Cell 96:667-676(1999).
RN [13]
RP -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by a
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation. Acts as coreceptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Found in promyelocytic cell.
CC -I- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
CC -I- PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X91492; CAA62796.1; -;
DR EMBL; U54994; AAC50598.1; -;
DR EMBL; U57840; AAB17071.1; -;
DR EMBL; U95626; AAB57793.1; -;
DR EMBL; U83326; AAC51797.1; -;
DR EMBL; AF011500; AAB65700.1; -;
DR EMBL; AF011501; AAB65701.1; -;
DR EMBL; AF011502; AAB65702.1; -;
DR EMBL; AF011503; AAB65703.1; -;
DR EMBL; AF011505; AAB65705.1; -;
DR EMBL; AF011506; AAB65706.1; -;
DR EMBL; AF011507; AAB65707.1; -;
DR EMBL; AF011508; AAB65708.1; -;
DR EMBL; AF011509; AAB65709.1; -;
DR EMBL; AF011510; AAB65710.1; -;
DR EMBL; AF011511; AAB65711.1; -;
DR EMBL; AF011512; AAB65712.1; -;
DR EMBL; AF011513; AAB65713.1; -;
DR EMBL; AF011514; AAB65714.1; -;
DR EMBL; AF011515; AAB65715.1; -;
DR EMBL; AF011516; AAB65716.1; -;
DR EMBL; AF011517; AAB65717.1; -;
DR EMBL; AF011518; AAB65718.1; -;
DR EMBL; AF011519; AAB65719.1; -;
DR EMBL; AF011520; AAB65720.1; -;
DR EMBL; AF011521; AAB65721.1; -;
DR EMBL; AF011522; AAB65722.1; -;
DR EMBL; AF011523; AAB65723.1; -;
DR EMBL; AF011524; AAB65724.1; -;
DR EMBL; AF011525; AAB65725.1; -;
DR EMBL; AF011526; AAB65726.1; -;
DR EMBL; AF011527; AAB65727.1; -;
DR EMBL; AF011528; AAB65728.1; -;
DR EMBL; AF011529; AAB65729.1; -;
DR EMBL; AF011530; AAB65730.1; -;
DR EMBL; AF011531; AAB65731.1; -;
DR EMBL; AF011532; AAB65732.1; -;
DR EMBL; AF011533; AAB65733.1; -;
DR EMBL; AF011534; AAB65734.1; -;
DR EMBL; AF011535; AAB65735.1; -;
DR EMBL; AF011536; AAB65736.1; -;
DR EMBL; AF011537; AAB65737.1; -;
DR EMBL; AF031237; AAB94735.1; -;
DR EMBL; AF052539; AAD18131.1; -;
DR EMBL; AY221093; AAO65971.1; -;
DR Genew; HGNC:1606; CCR5.
DR MIM; 601373; -;
DR GO; GO:0003768; C:Endosome; TAS.
DR GO; GO:0003687; C:integral to plasma membrane; TAS.
DR GO; GO:0016493; F:C-C chemokine receptor activity; NAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; ChkKinase_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Sulfation;
KW Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).

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FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).

Query Match
Best Local Similarity 99.7%; Score 1836; DB 1; Length 352;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Db 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLTGLYFGFSGIFPII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLTGLYFGFSGIFPII 120
Qy 121 LLTIDRYLAVHVAHFALKARTVTGGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVHVAHFALKARTVTGGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 2
CKR5 PANPA
ID CKR5 PANPA STANDARD; PRT; 352 AA.
AC P60574;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCRS).
GN Name=CCRS; Synonyms=CMKRS5;
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9597;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
CC -----
CC EMBL; AF17893; AAK43376.1; -
CC Pfam; PF00001; 7cm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
KW

```

```

FT TRANSMEM 1 30 Extracellular (Potential).
FT DOMAIN 31 58 1 (Potential).
FT TRANSMEM 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT TRANSMEM 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT TRANSMEM 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT TRANSMEM 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT TRANSMEM 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT TRANSMEM 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT TRANSMEM 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 BY similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
FT CARBOHYD 268 268 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 40539 MW; 4A33B698B80FE34C CRC64;

Query Match
Best Local Similarity 99.4%; Score 1830; DB 1; Length 352;
Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Db 1 MDYQVSSPIYDINYYTSPCKINVKQIAARLLPPLYSLSVFIQFVGNMVLILINCKR 60
Qy 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLTGLYFGFSGIFPII 120
Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLTGLYFGFSGIFPII 120
Qy 121 LLTIDRYLAVHVAHFALKARTVTGGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVHVAHFALKARTVTGGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFYSQVQFKNFQTLKIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 3
CKR5 PANTR
ID CKR5 PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 23-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCRS).
GN Name=CCRS; Synonyms=CMKRS5;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."

```

Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
[2]
SEQUENCE FROM N.A.
Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Wang G., Hahn B.,
Ho D.D.;
"HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
[4]
SEQUENCE FROM N.A.
MEDLINE=97426118; PubMed=9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
Hiv type 1 host.";
AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
[5]
SEQUENCE FROM N.A.
MEDLINE=98030115; PubMed=9430250;
Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
"Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
[6]
SEQUENCE FROM N.A.
Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and primate
phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC
-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC

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or send an email to license@isb-sib.ch).
CC

EMBL; AF005663; AAB62557.1; -
DR DR EMBL; U94329; AAB58446.1; -
DR DR EMBL; AF011542; AAB65742.1; -
DR DR EMBL; U97666; AAC51670.1; -
DR DR EMBL; AF013540; AAB65740.1; -
DR DR EMBL; U89797; AAC03717.1; -
DR DR EMBL; AF177894; AAK43377.1; -
DR DR InterPro; IPR002240; CC 5 receptor.
DR DR InterPro; IPR000355; Chk1 kinase receptor.
DR DR InterPro; IPR000276; GPCR_Rhodopsin.
DR DR Pfam; PF00001; 7tm1.1; 1.
DR DR PRINTS; PR00237; GPCRHHODPSN.
DR DR PROSITE; PS00237; G PROTEIN RECF F1_1; 1.
DR DR PROSITE; PS0262; G PROTEIN RECF F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT FT

FT	TRANSMEM	236	260	6 (Potential).
FT	DOMAIN	261	277	Extracellular (Potential).
FT	TRANSMEM	278	301	7 (Potential).
FT	DOMAIN	302	352	Cytoplasmic (Potential).
FT	DISULFID	101	178	By similarity.
FT	MOD_RSS	3	3	Sulfotyrosine (By similarity).
FT	MOD_RSS	10	10	Sulfotyrosine (By similarity).
FT	MOD_RSS	14	14	Sulfotyrosine (By similarity).
FT	MOD_RSS	15	15	Sulfotyrosine (By similarity).
FT	CARBOHYD	268	268	N-linked (GlcNAc...) (Potential).
FT	CONFLICT	123	123	T -> S (in Ref. 1).
SEQ	SEQUENCE	352 AA;	40539 MW;	4A33E698B0FE34C CRC64;
Query Match				
Best Local Similarity		99.4%;	Score 1830;	DB 1; Length 352;
Matches 349;		Conservative	2;	Mismatches 1; Indels 0; Gaps 0;
Qy	1	MDYQVSSPIYDINVTSEPCQKINVKQIARLLPPLYSLVFIFGFVGNMLVILLINCKR	60	
Db	1	MDYQVSSPIYDIDYITSEPCQKINVKQIARLLPPLYSLVFIFGFVGNMLVILLINCKR	60	
Qy	61	LKSMTDIYLLNLAIASDLFFLLTPVPWAHYLAAQWDGNTWCQLLTGLYFIFGFSGIFFII	120	
Db	61	LKSMTDIYLLNLAIASDLFFLLTPVPWAHYAAAQWDGNTWCQLLTGLYFIFGFSGIFFII	120	
Qy	121	LLTIDRYLVAVHAFALKARTVTFGVVTSVITWWAVFASLPGIITRSQKEGHYTCSS	180	
Db	121	LLTIDRYLAIHAFVAFALKARTVTFGVVTSVITWWAVFASLPGIITRSQKEGHYTCSS	180	
Qy	181	HFPSYQOFWKNFQTLKIVILGHVLPILVWVICYSGILKTLRCRKKRHRAVRLIFTI	240	
Db	181	HFPSYQOFWKNFQTLKIVILGHVLPILVWVICYSGILKTLRCRKKRHRAVRLIFTI	240	
Qy	241	MIYVFLFWAPYNTVLLINTQEFEGFLNCCSSNRLDQAMQVTFGLMTHCCINPIIYAFV	300	
Db	241	MIYVFLFWAPYNTVLLINTQEFEGFLNCCSSNRLDQAMQVTFGLMTHCCINPIIYAFV	300	
Qy	301	GEXPRNVLVFPKHKIAKPCCKCSITIQOBAPERASSVYTRSTGEOEISVGL	352	
Db	301	GEXPRNVLVFPKHKIAKPCCKCSITIQOBAPERASSVYTRSTGEOEISVGL	352	

RESULT 4

CCRS5_PONPA	STANDARD;	PRT;	352 AA.
ID	CCRS5_PONPA		
AC	P61756;		
DT	05-JUL-2004 (Rel. 44, Created)		
DT	05-JUL-2004 (Rel. 44, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DT	C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5) .		
DE	Name=CCR5; Synonyms=CMKBR5;		
OS	Pongo pygmaeus abelii (Sumatran orangutan) .		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.		
OX	NCBI_TaxID=9601;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=99416438; PubMed=10486970;		
RX	Zhang Y.-W., Ryder O.A., Zhang Y.-P.;		
RA	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";		
RL	Mol. Biol. Evol. 16:1145-1154(1999).		
CC	-I- MTP-1-beta and RANTES and subsequently transduces a signal by		
CC	increasing the intracellular calcium ions level. May play a role		
CC	in the control of granulocytic lineage proliferation or		
CC	differentiation.		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	contradict the copyright notice.		


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QY 241 MIVYFLWAPYNIIVLLNTFOEFGLNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFOEFGLNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNLYLVFFQKHAKRCKCCSIFQQAPEPARASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNLYLVFFQKHAKRCKCCSIFQQAPEPARASSVYTRSTGEQEISVGL 352

RESULT 6
Q71IT22
ID Q71IT22 PRELIMINARY; PRT; 352 AA.
AC Q71IT22
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-C chemokine receptor 5.
GN Name=CCR5;
OS Pongo pygmaeus pygmaeus (Bornean orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9602;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177900; AAK43383.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chk kinase receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF656A CRC64;

Query Match 99.1%; Score 1825; DB 2; Length 352;
Best Local Similarity 98.9%; Pred. No. 2e-104;
Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPTVDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
Db 1 MDYQVSSPTVDIDYTTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
QY 61 LKSNMTDILNLALSDILFLLTPVFAHYLAQWDFGNTWCQLLTGLYFTGFSGIFFII 120
Db 61 LKSNMTDILNLALSDILFLLTPVFAHYLAQWDFGNTWCQLLTGLYFTGFSGIFFII 120
QY 121 LLATIDRYLAIVHVAFLKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLATIDRYLAIVHVAFLKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQYQVKNFQTLKIVILGLVPLLVNVIYSGILKTLKCRNKKHRAVRLIFTI 240
Db 181 HPFYSQYQVKNFQTLKIVILGLVPLLVNVIYSGILKTLKCRNKKHRAVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFOEFGLNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFOEFGLNLCSSNRLDQAMQVETLGTWTHCCINPIIYAFV 300
QY 301 GEKFRNLYLVFFQKHAKRCKCCSIFQQAPEPARASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNLYLVFFQKHAKRCKCCSIFQQAPEPARASSVYTRSTGEQEISVGL 352
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RESULT 7
CKR5_GORGO
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN Name=CCR5; Synonyms=CMKBR5;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharzon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Feilner S.C., Farmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005659; AAB62553.1; -.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chk kinase receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT DOMAIN 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT DOMAIN 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;

Query Match 98.9%; Score 1820; DB 1; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;
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DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;

Query Match          98.9%; Score 1820; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
   |||||
Db 1 MDYQSSPTDYIDYITSEPCQTNVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
   |||||

QY 61 LKSMTDIYLLNLAIASDLFFLLTPFWAHYLAQWDFGNMTCOLLTGLYIFGFSGIFFII 120
   |||||
Db 61 LKSMTDIYLLNLAIASDLFFLLTPFWAHYLAQWDFGNMTCOLLTGLYIFGFSGIFFII 120
   |||||

QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
   |||||
Db 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
   |||||

QY 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKRRHRAVLIFTI 240
   |||||
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKRRHRAVLIFTI 240
   |||||

QY 241 MIVYFLFWAPYINVLNTQEFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFV 300
   |||||
Db 241 MIVYFLFWAPYINVLNTQEFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFV 300
   |||||

QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
   |||||
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
   |||||

RESULT 10
Q71TZ1
ID Q71TZ1 PRELIMINARY; PRT; 352 AA.
AC Q71TZ1; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE C-C chemokine receptor 5.
GN Name=CCRS;
OS Gorilla gorilla graueri (Eastern lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=46359;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF177902; AAK43385.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-c chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; GPCR_Rhodopsin.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;
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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;

Query Match          98.9%; Score 1820; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 4e-104;
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
   |||||
Db 1 MDYQSSPTDYIDYITSEPCQTNVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
   |||||

QY 61 LKSMTDIYLLNLAIASDLFFLLTPFWAHYLAQWDFGNMTCOLLTGLYIFGFSGIFFII 120
   |||||
Db 61 LKSMTDIYLLNLAIASDLFFLLTPFWAHYLAQWDFGNMTCOLLTGLYIFGFSGIFFII 120
   |||||

QY 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
   |||||
Db 121 LLTIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
   |||||

QY 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKRRHRAVLIFTI 240
   |||||
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRLCRNEKRRHRAVLIFTI 240
   |||||

QY 241 MIVYFLFWAPYINVLNTQEFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFV 300
   |||||
Db 241 MIVYFLFWAPYINVLNTQEFGLNCCSSNRDLQAMQVTTGLMTHCCINPIIYAFV 300
   |||||

QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
   |||||
Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
   |||||

RESULT 11
O18771
ID O18771 PRELIMINARY; PRT; 352 AA.
AC O18771; 1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCR5 receptor (Fragment).
GN Name=CCRS;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RT AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF011539; AAB65739.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-c chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; GPCR_Rhodopsin.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9F5EAC84 CRC64;
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SQ SEQUENCE 352 AA; 40466 MW; 3FFAC7ABAE1D4FB CRC64;
Query Match 98.8%; Score 1818; DB 2; Length 352;
Best Local Similarity 98.6%; Pred. No. 5.3e-104;
Matches 347; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGNMLVILINCKR 60
DB 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAARLLPPLSLVIFGFGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFGFSGIFFI 120
DB 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFGFSGIFFI 120
QY 121 LLTIDRYLAVHVA FALKARTVTFGVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVA FALKARTVTFGVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQFKNFQTKIVILGLVPLLVNMVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYSQVQFKNFQTKIVILGLVPLLVNMVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNI VLLNTFOEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNI VLLNTFOEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCFKCCSIFQEQAPERASSVYTRSTGEQBIISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCFKCCSIFQEQAPERASSVYTRSTGEQBIISVGL 352

RESULT 12
O18772 PRELIMINARY; PRT; 352 AA.
AC O18772;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCR5 receptor (Fragment).
GN Name=CCR5;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF011541; AAB65741.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON TER 352
SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 98.8%; Score 1818; DB 2; Length 352;

Best Local Similarity 98.6%; Pred. No. 5.3e-104;
Matches 347; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGNMLVILINCKR 60
DB 1 MDYQVSSPIYDIDYITSEPCQKINVKQIAARLLPPLSLVIFGFGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFGFSGIFFI 120
DB 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLA A QWDFGNTMCQLLTGLYFGFSGIFFI 120
QY 121 LLTIDRYLAVHVA FALKARTVTFGVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVA FALKARTVTFGVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQFKNFQTKIVILGLVPLLVNMVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYSQVQFKNFQTKIVILGLVPLLVNMVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNI VLLNTFOEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNI VLLNTFOEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCFKCCSIFQEQAPERASSVYTRSTGEQBIISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCFKCCSIFQEQAPERASSVYTRSTGEQBIISVGL 352

RESULT 13
Q9XS99 PRELIMINARY; PRT; 352 AA.
AC Q9XS99;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CC chemokine receptor 5.
GN Name=ccr5;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP MEDLINE=99210133; PubMed=10195758; DOI=10.1089/08922299311231;
RX Sakkena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF105291; AAD20560.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 98.7%; Score 1817; DB 2; Length 352;

Best Local Similarity 98.3%; Pred. No. 6.1e-104;
Matches 346; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLSLVIFGFGNMLVILINCKR 60

```
Db 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLAQWDFGNTMCOLLTLGLYFIFGFSGIFII 120
Db 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLAQWDFGNTMCOLLTLGLYFIFGFSGIFII 120
Qy 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVHAFALKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Qy 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Qy 301 GEKFRNLLVFFQKHIAKRFCKCSIFQQAEPARASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRFCKCSIFQQAEPARASSVYTRSTGEQISVGL 352

RESULT 14
CKR5 SEMEN STANDARD; PRT; 352 AA.
AC P61757;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS) .
GN Name=CCRS; Synonyms=CMKBR5;
OS Semnophthecus entellus (Hannuman langur) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Semnophthecus.
OX NCBI_TaxID=88029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC -----
DR EMBL; AF177896; AAK43379.1; -
DR PROSITE; PS00237; G-PROTEIN RECEPTOR 1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR 1; 2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).
```

```
FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT DOMAIN 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT DOMAIN 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD RES 3 3 Sulfotyrosine (By similarity).
FT MOD RES 10 10 Sulfotyrosine (By similarity).
FT MOD RES 14 14 Sulfotyrosine (By similarity).
FT MOD RES 15 15 Sulfotyrosine (By similarity).
FT CARBOHYD 268 268 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 98.6%; Score 1816; DB 1; Length 352;
Best Local Similarity 97.7%; Pred. No. 7e-104;
Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
Db 1 MDYQVSSPTDYDYITSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLAQWDFGNTMCOLLTLGLYFIFGFSGIFII 120
Db 61 LKSMTDIYLLNLAI SDFLLTVPFWAHYLAQWDFGNTMCOLLTLGLYFIFGFSGIFII 120
Qy 121 LLTIDRYLAVVHAFALKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVHAFALKARTVTFGVVTSVITVWVAVFASLPGLIIFTRSQEGLHYTCSS 180
Qy 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPFSYQYQWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYINVLNLTQEFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
Qy 301 GEKFRNLLVFFQKHIAKRFCKCSIFQQAEPARASSVYTRSTGEQISVGL 352
Db 301 GEKFRNLLVFFQKHIAKRFCKCSIFQQAEPARASSVYTRSTGEQISVGL 352

RESULT 15
CKR5 TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS) .
GN Name=CCRS; Synonyms=CMKBR5;
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC -----
```

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EMBL; AF075443; AAD19855.1; -
InterPro; IPR002240; CC 5. receptor.
InterPro; IPR000355; Chkline receptor.
InterPro; IPR000276; GPCR_Rhodopsin.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCR_Rhodopsin.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT DOMAIN 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 89 2 (Potential).
FT DOMAIN 90 102 Extracellular (Potential).
FT TRANSMEM 103 124 3 (Potential).
FT DOMAIN 125 141 Cytoplasmic (Potential).
FT TRANSMEM 142 166 4 (Potential).
FT DOMAIN 167 198 Extracellular (Potential).
FT TRANSMEM 199 218 5 (Potential).
FT DOMAIN 219 235 Cytoplasmic (Potential).
FT TRANSMEM 236 260 6 (Potential).
FT DOMAIN 261 277 Extracellular (Potential).
FT TRANSMEM 278 301 7 (Potential).
FT DOMAIN 302 352 Cytoplasmic (Potential).
FT DISULFID 101 178 By similarity.
FT MOD_RES 3 3 Sulfotyrosine (By similarity).
FT MOD_RES 10 10 Sulfotyrosine (By similarity).
FT MOD_RES 14 14 Sulfotyrosine (By similarity).
FT MOD_RES 15 15 Sulfotyrosine (By similarity).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938f CRC64;

Query Match 98.6%; Score 1816; DB 1; Length 352;
Best Local Similarity 97.7%; Pred. No. 7e-104;
Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTSEPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILILNCKR 60
DB 1 MDYQVSSPTDIDYITSEPCKQNVKQIAARLLPPLYSLVIFGFGVGNILVILILNCKR 60
QY 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIFGFGSIFFI 120
DB 61 LKSMTDIYLLNLALSDFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIFGFGSIFFI 120
QY 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLVAVHAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPPYSQYQFNQFQTLKIVILGLVPLLVMIYCYSGILKTLRCRNEKKRHRAVRLIFTI 240
DB 181 HPPYSQYQFNQFQTLKIVILGLVPLLVMIYCYSGILKTLRCRNEKKRHRAVRLIFTI 240
QY 241 MIVVFLFWAPNIVLLNTFQEPFGLNCSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
DB 241 MIVVFLFWAPNIVLLNTFQEPFGLNCSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHAKRFCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHAKRFCKCSIFQEQAPERASSVYTRSTGEQISVGL 352

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Search completed: October 3, 2005, 07:45:50
Job time : 100 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 06:08:13 ; Search time 90 Seconds
(without alignments)

1512.663 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDVQVSPYDINYYTSEPC.....ERASSVYTRTGQEIISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	100.0	371	2	AAW23834 Human CC
2	1836	99.7	352	2	AAW27407 Human CCR
3	1836	99.7	352	2	AAW27123 Human che
4	1836	99.7	352	2	AAW23835 Human CC
5	1836	99.7	352	2	AAW88232 Human CCR
6	1836	99.7	352	4	AAW80111 Human CCR
7	1836	99.7	352	4	AAW04321 Human che
8	1836	99.7	352	4	AAW83354 Human CCR
9	1836	99.7	352	4	AAW82948 Human HIV
10	1836	99.7	352	5	AAW52828 Human CC
11	1836	99.7	352	5	ABW08343 Human che
12	1836	99.7	352	6	ABW58602 Human can
13	1836	99.7	352	6	AAO29514 Human C-C
14	1836	99.7	352	6	ABP97728 Amino aci
15	1836	99.7	352	6	ABP81933 Human C-C
16	1836	99.7	352	7	ADC03341 Human che
17	1836	99.7	352	7	ADP44882 Human CC
18	1836	99.7	352	7	ADK17356 Human CCR
19	1836	99.7	352	7	ADP65192 Human che
20	1836	99.7	352	8	ADG42778 Human CC
21	1836	99.7	352	8	ADH60807 Human CC-
22	1836	99.7	352	8	ADM35887 Human che
23	1836	99.7	352	8	ADO29227 Human GPC
24	1836	99.7	352	8	ADP12403 Protein e
25	1836	99.7	352	8	ADO19578 Human PRO

26	1836	99.7	352	8	ADQ21275 Human sof
27	1836	99.7	352	8	ADP24004 PRO polyp
28	1836	99.7	352	8	ADT90847 Human che
29	1836	99.7	439	2	AAV41280 Fusion pr
30	1833	99.6	363	8	ADR88809 Human G p
31	1830	99.4	352	4	ABW56342 Non-endog
32	1830	99.4	352	5	AAW52829 Human CCR
33	1828	99.3	352	4	AAE07048 Human G-p
34	1828	99.3	352	4	AAE07039 Human G-p
35	1828	99.3	352	4	AAW46858 Human HDG
36	1828	99.3	352	5	AAU97152 Human G-p
37	1828	99.3	352	5	ABG70597 Human G-p
38	1828	99.3	352	5	ABG92883 Human imm
39	1828	99.3	352	5	AAE25811 Human G-p
40	1828	99.3	352	5	ABW81054 G-protein
41	1828	99.3	352	6	ABG75540 Human G-p
42	1828	99.3	352	6	ABU61654 Human G-p
43	1828	99.3	352	7	ADF72142 Human G-p
44	1828	99.3	352	8	ADP86210 Human G-p
45	1828	99.3	352	8	ADR16259 Human G-p

ALIGNMENTS

RESULT 1
AAW23834
ID AAW23834 standard; protein; 371 AA.
XX AC AAW23834;
XX XX
DT 08-JUN-1998 (first entry)
XX XX
DE Human CC chemokine receptor 5 (CCR5) A127V variant.
XX XX
KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX XX
OS Homo sapiens.
XX XX
PH Key Location/Qualifiers
FT Domain 48..74
FT /label= I
FT /note= "transmembrane domain"
FT Domain 123..145
FT /label= III
FT /note= "transmembrane domain"
FT Domain 162..190
FT /label= IV
FT /note= "transmembrane domain"
FT Domain 213..238
FT /label= V
FT /note= "transmembrane domain"
FT Domain 257..277
FT /label= VI
FT /note= "transmembrane domain"
FT Domain 296..319
FT /label= VII
FT /note= "transmembrane domain"
WO9745543-A2.
04-DEC-1997.
28-MAY-1997; 97WO-US009586.
28-MAY-1996; 96US-0018508P.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
Broder CC, Kennedy PE;
XX XX

DR WPI; 1998-032650/03.
 DR N-PSDB; AAT76919.
 XX
 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 XX
 PS Example 1; Fig 1B; 70pp; English.
 XX
 CC This protein sequence comprises an Alal27Leu variant of a novel human
 CC macrophage-selective CC chemokine receptor (see also AAW23835) that has
 CC been designated CCR5. The sequence was deduced from an isolated cDNA
 CC clone (see AAT76919). The conservative variation should not affect the
 CC activity of CCR5. The susceptibility of human macrophages to HIV
 CC infection depends on cell surface expression of CD4 and CCR5. CCR5 is a
 CC member of the 7-transmembrane superfamily of G-protein coupled cell
 CC surface molecules. It plays an essential role in the membrane fusion step
 CC of infection by some HIV isolates. The establishment of stable, non-human
 CC cell lines and transgenic mammals having cells that coexpress human CD4
 CC and CCR5 provides valuable tools for research of HIV infection.
 CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents
 CC capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 SQ Sequence 371 AA;
 Query Match 100.0%; Score 1841; DB 2; Length 371;
 Best Local Similarity 100.0%; Pred. No. 9.3e-195;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
 DB 20 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 79
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYIFGPGSGIFFII 120
 DB 80 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYIFGPGSGIFFII 139
 QY 121 LITIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 DB 140 LITIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 199
 QY 181 HPFSYQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 DB 200 HPFSYQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKKHRAVRLIFTI 259
 QY 241 MIVYFLFWAPYNIYLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 DB 260 MIVYFLFWAPYNIYLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 319
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEISVGL 352
 DB 320 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEISVGL 371
 RESULT 2
 AAW27407
 ID AAW27407 standard; protein; 352 AA.
 XX
 AC AAW27407;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human CCR5.
 XX
 KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX
 OS Homo sapiens.
 XX

PN W09732019-A2.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-BE0000023.
 XX
 PR 01-MAR-1996; 96EP-00870021.
 PR 06-AUG-1996; 96EP-00870102.
 XX
 PA (EURO-) EUROSREEN SA.
 XX
 PI Samson M, Parmentier M, Vassart G, Libert F;
 XX WPI; 1997-479829/44.
 DR N-PSDB; AAT90117.
 XX
 PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX
 PS Claim 4; Fig 1b-c; 94pp; English.
 XX
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX
 SQ Sequence 352 AA;
 Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYIFGPGSGIFFII 120
 DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYIFGPGSGIFFII 120
 QY 121 LITIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LITIDRYLAVVHAFVFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 QY 181 HPFSYQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 DB 181 HPFSYQYQFWKNFQTLKIVILGLVPLLVWVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
 QY 241 MIVYFLFWAPYNIYLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIYLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
 QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEISVGL 352
 DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGGEISVGL 352
 RESULT 3
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX
 AC AAW27123;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
KW modulator; antibody; human.
XX Homo sapiens.
XX Key: Location/Qualifiers
FH 1. .32
FT Domain /label= Extracellular_domain
FT 56. .67
FT Domain /label= Intracellular_domain
FT 89. .112
FT Domain /label= Extracellular_domain
FT 125. .145
FT Domain /label= Intracellular_domain
FT 166. .191
FT Domain /label= Extracellular_domain
FT 213. .235
FT Domain /label= Intracellular_domain
FT 259. .280
FT Domain /label= Extracellular_domain
FT 301. .352
FT Domain /label= Intracellular_domain
XX WO9722698-A2.
XX 26-JUN-1997.
XX 20-DEC-1996; 96WO-US020759.
XX 20-DEC-1995; 95US-00575967.
XX 07-JUN-1996; 96US-00661393.
XX (ICOS-) ICOS CORP.
XX Gray PW, Schweickart VL, Raport CJ;
PI WPI; 1997-341689/31.
DR N-PSDB; AAT85161.
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
PT tumours, viral infections, auto-immune diseases, etc.
XX Claim 16; Page 47-48; 65pp; English.
XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
CC G protein coupled receptor that is involved in leukocyte trafficking. Its
CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor
CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
CC and their polypeptide fragments can be produced in transformed host
CC cells. The receptors, peptides comprising one or more of the
CC extracellular or intracellular domains, and anti-receptor antibodies can
CC be used to modulate receptor activities, particularly ligand and G
CC protein binding, and are potentially useful in the treatment
CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune response,
CC abnormal haematopoietic processes etc
XX Sequence 352 AA;
SQ
Query Match 99.7%; Score 1836; DB 2; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINVTSEPCQKNVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINVTSEPCQKNVKQIAARLLPPLSLVIFGFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAQWDFGNTMCQLLTGLYFTGFSGIFFII 120

Db 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
QY 121 LLTIDRYLAVVHAFVFAKARTVTGGVTSVITWVAVFASLPGIIPTRSOKEGHLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVFAKARTVTGGVTSVITWVAVFASLPGIIPTRSOKEGHLHYTCSS 180
QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVIQYSGILKTLRLCRNEKKRHRAVRLIFTI 240
Db 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVIQYSGILKTLRLCRNEKKRHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIYLLNTFQEPFGLNCCSSNRLDOAMOVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIYLLNTFQEPFGLNCCSSNRLDOAMOVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNVLVFFQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQDISVGL 352
Db 301 GEKFRNVLVFFQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQDISVGL 352
RESULT 4
AAW23835
ID AAW23835 standard; protein; 352 AA.
XX AAW23835;
XX 08-JUN-1998 (first entry)
XX Human CC chemokine receptor 5 (CCR5).
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX Homo sapiens.
XX Key: Location/Qualifiers
FH 29. .55
FT Domain /label= I
FT /note= "transmembrane domain"
FT 104. .126
FT Domain /label= III
FT /note= "transmembrane domain"
FT 109. .120
FT Region /note= "extracellular loop-1 (Claim 19)"
FT 143. .171
FT Domain /label= IV
FT /note= "transmembrane domain"
FT 187. .210
FT Region /note= "extracellular loop-2 (Claim 19)"
FT 194. .219
FT Domain /label= V
FT /note= "transmembrane domain"
FT 238. .258
FT Domain /label= VI
FT /note= "transmembrane domain"
FT 261. .276
FT Region /note= "extracellular loop-3 (Claim 19)"
FT 277. .300
FT Domain /label= VII
FT /note= "transmembrane domain"
XX WO9745543-A2.
XX 04-DEC-1997.
XX 28-MAY-1997; 97WO-US009586.
XX 28-MAY-1996; 96US-0018508P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
PI Broder CC, Kennedy PE;

XX WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 FT
 XX PS
 XX Claim 68; Fig 1C; 70pp; English.
 XX
 CC This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 XX SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
 Db 61 LKSMTDIYLLNLAISDLFFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
 QY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVNVIYSGILKTLRCRNEKRRHRAVRLIFTI 240
 Db 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVNVIYSGILKTLRCRNEKRRHRAVRLIFTI 240
 QY 241 MIVYFLWAPYINVLNLTNTPQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 Db 241 MIVYFLWAPYINVLNLTNTPQEFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
 QY 301 GEKFRNVLVFFQKHAKRCKCSIFQQAPEPRASSVYTRSTGEQEIISVGL 352
 Db 301 GEKFRNVLVFFQKHAKRCKCSIFQQAPEPRASSVYTRSTGEQEIISVGL 352

RESULT 5
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE HIV-1 co-receptor CCR5.
 XX
 KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT

FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT 103..124
 FT /note= "transmembrane domain 3"
 FT 142..167
 FT /note= "transmembrane domain 4"
 FT 200..223
 FT /note= "transmembrane domain 5"
 FT 236..260
 FT /note= "transmembrane domain 6"
 FT 275..301
 FT /note= "transmembrane domain 7"
 XX
 XX W09854317-A1.
 PN
 XX 03-DEC-1998.
 PD
 XX
 XX 29-MAY-1998; 98WO-BP003437.
 PF
 XX 30-MAY-1997; 97US-0048057P.
 PR
 XX
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PA
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 PI WPI; 1999-059835/05.
 XX N-PSDB; AAV84126.
 DR
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 FT
 XX Disclosure; Page 34-35; 55pp; English.
 PS
 XX This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW88231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 XX
 XX SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINVTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
 Db 61 LKSMTDIYLLNLAISDLFFLLTPFPWAHYLAAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
 QY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 Db 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVNVIYSGILKTLRCRNEKRRHRAVRLIFTI 240

Db 181 HFPYSQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
 Qy 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFPQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNYLLVFPQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 6
 AAG80111
 ID AAG80111 standard; protein; 352 AA.
 XX AC
 XX AAG80111;
 DT 17-JAN-2002 (first entry)
 XX DE
 DE Human CCR5 protein.
 XX KW
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX KW
 OS Homo sapiens.
 XX FN
 FN WO200172830-A2.
 XX PD
 PD 04-OCT-2001.
 XX PF
 PF 02-APR-2001; 2001WO-EP003708.
 XX PR
 PR 31-MAR-2000; 2000DB-01016013.
 XX PA
 PA (IPFP-) IPF PHARM GMBH.
 XX PA (FORS/) FORSMANN U.
 XX PI
 PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
 XX WPI; 2001-626256/72.
 XX DR
 DR Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX PS
 PS Disclosure; Page 10; 26pp; German.
 XX CC
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX SQ
 SQ Sequence 352 AA;

Query Match 59.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 59.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIIFGVGNMLVILINCKR 60
 Db 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIIFGVGNMLVILINCKR 60
 Qy 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIPFII 120
 Db 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIPFII 120
 Qy 121 LLTIIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 Db 121 LLTIIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
 Qy 181 HFPYSQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
 Db 181 HFPYSQVQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKRRHRAVRLIFTI 240
 Qy 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLWAPYNIIVLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFPQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNYLLVFPQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 7
 AAE04321
 ID AAE04321 standard; protein; 352 AA.
 XX AC
 XX AAE04321;
 DT 04-SEP-2001 (first entry)
 XX DE
 DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.
 XX KW
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR-5; envelope glycoprotein; anti-HIV.
 XX OS
 OS Homo sapiens.
 XX PN
 PN US6258527-B1.
 XX PD
 PD 10-JUL-2001.
 XX PF
 PF 21-MAY-1997; 97US-00861105.
 XX PR
 PR 20-MAY-1996; 96US-0017157P.
 PR 19-JUN-1996; 96US-0020043P.
 PR 19-MAY-1997; 97US-00858660.
 XX PA
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX PA (UUNY) UNIV NEW YORK STATE.
 XX PI
 PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
 XX WPI; 2001-417127/44.
 DR N-PSDB; AAD08577.
 XX PT
 PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 XX HIV.
 PS Disclosure; Col 47-50; 37pp; English.
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of

CC HIV into transformed mammalian cell or for identifying a human chemokine
CC receptor that facilitates the infection of a particular HIV strain into
CC the transformed mammalian cell. Compounds identified can be used to treat
CC cellular dysfunction and to prevent or combat HIV infection. The present
CC sequence is a human chemokine receptor (CCR), CC-CCR-5 related protein.
CC CC-CCR-5 is the principal cofactor for entry mediated by the envelope
CC glycoproteins of primary macrophage-tropic strains of HIV-1
XX
XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
QY 61 LKSMTDIYLNLAIISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFFSGIFFII 120
DB 61 LKSMTDIYLNLAIISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFFSGIFFII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLWPAPYINVLILNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWPAPYINVLILNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 8
AAB83354
ID AAB83354 standard; protein; 352 AA.
XX
AC AAB83354;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human CCR5 protein sequence.
XX
KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
KW human immunodeficiency virus; anti-inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN EPI1118858-A2.
XX
PD 25-JUL-2001.
XX
PF 03-JAN-2001; 2001EP-00300020.
XX
PR 12-JAN-2000; 2000GB-00000659.
PR 12-JAN-2000; 2000GB-00000661.
PR 12-JAN-2000; 2000GB-00000663.
XX
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
PI Dobbs S, Perros M, Rickett GA;
XX
DR WPI; 2001-477088/52.
DR N-PSDB; AAF87099.
XX
PT Determining if an agent can modulate CCR5-gp120 interaction, comprises

PT incubating the agent with CCR5 and gp120 and determining if the agent
modulates the interaction.
XX
PS Claim 1; Page 110; 113pp; English.
XX

CC This sequence represents the human CCR5 protein sequence. The invention
relates to a method for determining whether an agent is capable of
modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
with gp120, comprising incubating the agent with CCR5 and gp120 and
determining whether the agent modulates the interaction, where gp120 is
associated with CD4, and where the interaction is a low affinity binding.
CC The method is used to identify an agent capable of modulating the
interaction of CCR5 with gp120. An agent identified by the method is used
to prepare a pharmaceutical composition for the treatment of a disease or
condition associated with CCR5 and gp120 interaction, to treat a subject
with a disease or condition associated with CCR5 and gp120 interaction,
and for preparing a pharmaceutical for treating human immunodeficiency
virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
is commercially useful, amenable to high throughput screening, and
detects interaction of gp120 with cells expressing only CCR5

SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCKINVKQIAARLLPPLYSLVFIFFGVGNMVLILINCKR 60
QY 61 LKSMTDIYLNLAIISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFFSGIFFII 120
DB 61 LKSMTDIYLNLAIISDLFFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFFSGIFFII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKHRAVRLIFTI 240
DB 181 HFPYSQYQFWKNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIVYFLWPAPYINVLILNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWPAPYINVLILNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 9

AAB82948
ID AAB82948 standard; protein; 352 AA.
XX
AC AAB82948;
XX
DT 21-DEC-2001 (first entry)
XX
DE Human HIV-1 co-receptor CCR5.
XX
KW CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
KW infection; therapy; vaccine; anti-HIV-1.
XX
OS Homo sapiens.
XX
PI Key Location/Qualifiers
FT Binding-site 2..18
FT /note= "binds to HIV-1 gp120"
XX
PN WO200164710-A2.
XX

PD 07-SEP-2001.
XX 28-FEB-2001; 2001WO-US006699.
XX 29-FEB-2000; 2000US-0185667P.
PR 19-MAY-2000; 2000US-0205839P.
PR 07-FEB-2001; 2001US-0267231P.
XX (PROG-) PROGENICS PHARM INC.
PA (AARO-) AARON DIAMOND AIDS RES CENT.
XX Dragic T, Olson WC;
XX WPI; 2001-611273/70.
DR N-PSDB; AAH26903.
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
PT receptor) amino terminal domain including negatively charged and two
PT sulfated tyrosine residues is useful for treating HIV infection in
PT humans.
XX Claim 1; Page 30; 163pp; English.
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
CC site that determines the specificity of the interaction between CCR5 and
CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
CC CCR5 N-terminus is required for gp120 binding and may critically modulate
CC the susceptibility of target cells to HIV-1 infection in vivo. The
CC invention provides claimed sulfated peptides (see AAB82947) that are
CC based on the CCR5 N-terminal region and which are effective for
CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
CC cells from becoming infected with HIV, of treating a subject whose CD4+
CC cells are infected with HIV, and of identifying an agent which inhibits
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
CC out in a subject, especially a human, infected (therapeutic method), not
CC infected with HIV (prophylactic method), or in a subject who is not
CC infected with, but has been exposed to, HIV
XX
SQ Sequence 352 AA;
Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGHLYTCSS 180
DB 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGHLYTCSS 180
QY 181 HFPYSQYQFKNQFOTLKIVILGLVPLLVVVICYSGLIKTLRCNKKHRAVRLIFTI 240
DB 181 HFPYSQYQFKNQFOTLKIVILGLVPLLVVVICYSGLIKTLRCNKKHRAVRLIFTI 240
QY 241 MIVYFLFWAPNIVILLANTQEPFLGNNCSSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPNIVILLANTQEPFLGNNCSSNRLDQAMQVTEFLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCKCSIFQEQAPERASSVYTRSTGEQISVGL 352

RESULT 10
AAM52828

ID AAM52828 standard; protein; 352 AA.
XX AAM52828;
XX 22-FEB-2002 (first entry)
XX Human CC chemokine receptor 5 (CCR5).
XX CCR5; CC chemokine receptor 5; human; HIV infection;
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW drug screening; identification.
XX Homo sapiens.
XX WO200171346-A2.
XX 27-SEP-2001.
XX 21-MAR-2001; 2001WO-US009155.
XX 21-MAR-2000; 2000US-0190946P.
PR 21-MAR-2000; 2000US-0190946P.
PR 21-MAR-2000; 2000US-0191299P.
PR 20-MAR-2001; 2001US-00813448.
PR 20-MAR-2001; 2001US-00813651.
XX 20-MAR-2001; 2001US-00813653.
XX (CONS-) CONSENSUS PHARM INC.
XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
PI WPI; 2002-010610/01.
DR N-PSDB; ABA02317.
XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT comprises binding a molecule from library to a molecule having binding
PT property corresponding to CCR5 and identifying bound molecule.
XX Example 3; Fig 4A; 50pp; English.
XX The invention relates to a method for identifying a binding compound for
CC chemokine receptor 5 (CCR5). The method involves screening a library
CC of test molecules (particularly peptides) with immobilised CCR5, and then
CC identifying those molecules which bind. The invention also relates to
CC CCR5-binding molecules identified using the method of the invention, a
CC methods for identifying consensus motifs for CCR5-binding peptides, a
CC transfer vector encoding tagged CCR5, a computer-aided methods for
CC determining the relative binding affinity of a test molecule to CCR5 and
CC a computer aided drug screening assay that utilises the three-dimensional
CC structure of CCR5. Compounds identified using the methods of the
CC invention are useful for treating or preventing HIV (human
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
CC syndrome) in a patient. The methods of the invention may also be used to
CC identify agonists or antagonists of the interaction of CCR5 with its
CC natural ligand, and to determine a binding motif for CCR5. The present
CC sequence represents human CCR5
XX
SQ Sequence 352 AA;
Query Match 99.7%; Score 1836; DB 5; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIFFII 120
QY 121 LLTIDRYLAVHVAFFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGHLYTCSS 180

Db 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
 Qy 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKRCNEKKGHRVRLIFTI 240
 Db 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKRCNEKKGHRVRLIFTI 240
 Qy 241 MIVYFLFWAPYINVLNLTQFEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 Db 241 MIVYFLFWAPYINVLNLTQFEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300
 Qy 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 11

ABB08343
 ID ABB08343 standard; protein; 352 AA.

XX ABB08343;

DT 18-JUN-2002 (first entry)

XX Human chemokine (C-C motif) receptor 5 polypeptide.

XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 55

FT /label= Leu, Gln

FT Misc-difference 182

FT /label= Phe, Leu

FT Misc-difference 223

FT /label= Arg, Gln

XX WO200177125-A2.

XX 18-OCT-2001.

XX 04-APR-2001; 2001WO-US010708.

XX 05-APR-2000; 2000US-0194361P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Klieem SE, Koshy B;

XX WPI; 2002-041282/05.

XX N-PSDB; ABA97318, ABA97319.

XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful
 FT to diagnose and treat diseases associated with its abnormal expression or
 FT function, including human immunodeficiency virus-1 infection.

XX Claim 29; Fig 3; 61pp; English.

XX The present sequence is that of a polypeptide encoded by the human
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5
 CC gene of an individual by determining if the individual has one of the
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.
 CC The specification also describes an isolated polynucleotide comprising a
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5
 CC gene sequence and comprises an isogene defined by a haplotype described
 CC in the specification and its encoded polypeptide. The methods of the
 CC invention are useful to diagnose and develop treatment for diseases
 CC associated with abnormal expression or function of the gene. the CCR5

CC isogenes and the screened compounds are useful for treating human
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired
 CC immunodeficiency syndrome (AIDS). The invention has antiviral
 CC applications. The specification describes genotyping the CCR5 gene of an
 CC individual; predicting a haplotype pair for the CCR5 gene of an
 CC individual; identifying an association between a trait and a haplotype or
 CC haplotype pair of the CCR5 gene. The specification describes a
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5
 CC polymorphism; a recombinant non-human organism transformed with CCR5
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;
 CC an isolated antibody specific for the CCR5 polypeptide and a method for
 CC screening drugs targeting the CCR5 polypeptide

XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 5; Length 352;

Best Local Similarity 99.7%; Pred. No. 3.1e-194;

Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60

Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFVGNMLVILINCKR 60

Qy 61 LKSMTDIYLLNLAISDLPLLTVPFWAHYLAQWDRGNTWCOLLTCLYFIQFSGIFFII 120

Db 61 LKSMTDIYLLNLAISDLPLLTVPFWAHYLAQWDRGNTWCOLLTCLYFIQFSGIFFII 120

Qy 121 LUTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

Db 121 LUTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

Qy 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKRCNEKKGHRVRLIFTI 240

Db 181 HFPYSQYQFKNFQTLKIVILGLVPLLVVVICYSGLKTLKRCNEKKGHRVRLIFTI 240

Qy 241 MIVYFLFWAPYINVLNLTQFEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300

Db 241 MIVYFLFWAPYINVLNLTQFEPFGLNCCSSNRLDQAMQVETLGTWTHCCINPIYAFV 300

Qy 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

Db 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 12

ABR58602

ID ABR58602 standard; protein; 352 AA.

XX ABR58602;

XX 09-JUL-2003 (first entry)

XX Human cancer related protein SEQ ID NO:259.

XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.

XX Homo sapiens.

XX WO2003025138-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-US029560.

XX 17-SEP-2001; 2001US-0323469P.

XX 20-SEP-2001; 2001US-0323887P.

XX 13-NOV-2001; 2001US-0350666P.

XX 08-FEB-2002; 2002US-0355145P.

XX 08-FEB-2002; 2002US-0355257P.

XX 12-APR-2002; 2002US-0372246P.

XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnik A;
 XX WPI; 2003-354600/33.
 DR N-PSDB; ACC72740.
 XX
 PT New genes that are up-regulated or down-regulated in cancers, useful as
 markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
 therapeutic targets for screening drugs for treating these diseases.
 XX
 PS Claim 12; Page 745; 767pp; English.
 XX
 CC The present invention describes an isolated nucleic acid molecule, which
 CC comprises the sequence of any of the genes that are up-regulated or down-
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
 CC related gene nucleotide sequences which encode the proteins given in
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or
 CC absence of a pathological cell in a patient; (2) an expression vector
 CC comprising a nucleic acid molecule described above; (3) a host cell
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
 CC of (4); (6) specifically targeting a compound to a pathological cell in a
 CC patient by administering to the patient the antibody above; and (7) a
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or
 CC therapeutic targets. In particular, the nucleic acid is useful for
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in
 CC drug screening, particularly for identifying agents for treating these
 CC pathologies
 XX
 SQ Sequence 352 AA;
 Query Match 99.7%; Score 1836; DB 6; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLSLVFIQFGVGNMLVILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLSLVFIQFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIQFGSIFPII 120
 DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIQFGSIFPII 120
 QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 DB 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
 DB 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
 QY 241 MIVYFLFWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
 QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352
 DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352
 RESULT 13
 ID AAO29514 standard; protein; 352 AA.
 XX AAO29514;
 XX 27-AUG-2003 (first entry)
 DT
 XX

DE Human C-C chemokine receptor type 5 (333) protein.
 XX Human; urological disorder; stress urinary incontinence; prostate cancer;
 KW benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
 KW overflow urinary incontinence; gene therapy; nephrotropic; prostatitis;
 KW kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2003039475-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-US035824.
 XX
 PR 07-NOV-2001; 2001US-0344552P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Silos-Santiago I;
 XX
 DR WPI; 2003-449396/42.
 DR N-PSDB; AAL59912.
 XX
 PT Identifying a compound, capable of treating urological disorder e.g.,
 PT benign prostatic hyperplasia, by assaying the ability of the compound to
 PT modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or
 PT polypeptide activity.
 XX
 PS Disclosure; Page 81; 87pp; English.
 XX
 CC The invention relates to a method for treating a urological disorder
 CC which comprises assaying the ability of the compound to modulate 313,
 CC 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide
 CC activity. The method is useful for identifying a compound for treating an
 CC urological disorder comprising urinary incontinence e.g., overactive/
 CC oversensitive bladder, overflow urinary incontinence, stress urinary
 CC incontinence caused by dysfunction of the bladder, urethra or central/
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
 CC prostate cancer or kidney disorders. It is also used in gene therapy. The
 CC present sequence is human C-C chemokine receptor type 5 (CCR5; 333)
 CC protein. This sequence is used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;
 Query Match 99.7%; Score 1836; DB 6; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLSLVFIQFGVGNMLVILINCKR 60
 DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLSLVFIQFGVGNMLVILINCKR 60
 QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIQFGSIFPII 120
 DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTMCQLLTGLYFIQFGSIFPII 120
 QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 DB 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
 QY 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
 DB 181 HPFYSQYQFQWKNFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKGHRVRLIFTI 240
 QY 241 MIVYFLFWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
 DB 241 MIVYFLFWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV 300
 QY 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352
 DB 301 GEKFRNLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQISVGL 352

```
RESULT 14
ABP97728
ID ABP97728 standard; protein; 352 AA.
XX
XX AC ABP97728;
XX
XX 28-MAY-2003 (first entry)
XX
XX DE Amino acid sequence of human chemokine receptor CCR5.
XX
XX KW Human; chemokine receptor; CCR5; viral infection; surface protein;
XX KW respiratory virus infection; respiratory syncytial virus infection;
XX KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
XX OS Homo sapiens.
XX
XX PN WO2003014153-A2.
XX
XX PD 20-FEB-2003.
XX
XX PF 12-AUG-2002; 2002WO-CA001248.
XX
XX PR 10-AUG-2001; 2001US-0311088P.
XX
XX PA (TOPI-) TOPIGEN PHARM INC.
XX
XX PI Renzi P, Zemzoui K;
XX
XX DR WPI; 2003-256541/25.
XX
XX DR N-PSDB; ABZ68881.
XX
XX PT Modulating viral infection of a cell, for treating or preventing
XX PT respiratory virus infections, bronchitis, pneumonia or asthma, by
XX PT modulating a binding interaction between a cell chemokine-receptor and a
XX PT surface protein of the virus.
XX
XX PS Disclosure; Page 96-98; 120pp; English.
XX
XX CC The present sequence represents human chemokine receptor CCR5. The
XX CC specification describes a method for modulating viral infection of a
XX CC cell. The method comprises modulating a binding interaction between a
XX CC cell chemokine-receptor and a surface protein of the virus. The proviso
XX CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
XX CC not HIV. The method is useful for treating or preventing respiratory
XX CC virus infection in vertebrates, more particularly respiratory syncytial
XX CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
XX CC bronchitis, pneumonia or asthma
XX
XX SQ Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 6; Length 352;
Best Local Similarity 99.7%; Pred. No. 3.1e-194;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINVTSEPCQKINVKQIARLLPPLYSLVFIQFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINVTSEPCQKINVKQIARLLPPLYSLVFIQFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
DB 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
QY 121 LLTIDRYLAVVHAFALKARTVTFGVVTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAFALKARTVTFGVVTVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQFWNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVLIFTI 240
DB 181 HPFYSQVQFWNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKRRHRAVLIFTI 240
QY 241 MIYVYFLWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
DB 241 MIYVYFLWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
```

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 352 AA;

Query Match		99.7%;	Score 1836;	DB 6;	Length 352;
Best Local Similarity		99.7%;	Pred. No. 3.1e-194;		
Matches 351;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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Db	1	MDYQVSSPIYDINTYTSPECKINVKQIAARLLPPLYSLVPIFGVGNMLVILILNCKR	60		
Qy	61	LKSMTDIYLLNLALSDFELLTPFMAHYLAQAQWDFGNMCOQLTGLYFIFGFSGIFFII	120		
Db	61	LKSMTDIYLLNLALSDFELLTPFMAHYLAQAQWDFGNMCOQLTGLYFIFGFSGIFFII	120		
Qy	121	LLTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS	180		
Db	121	LLTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS	180		
Qy	181	HFYSQYQFWKNFOTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKRHRAVRLIFTI	240		
Db	181	HFYSQYQFWKNFOTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKRHRAVRLIFTI	240		
Qy	241	MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVTEGLMTHCCINPIIYAFV	300		
Db	241	MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVTEGLMTHCCINPIIYAFV	300		
Qy	301	GEKFRNLLVFFQKHAKRCCKCSIFQQEAPERASSVYTRSTGEQEISVGL	352		
Db	301	GEKFRNLLVFFQKHAKRCCKCSIFQQEAPERASSVYTRSTGEQEISVGL	352		

Search completed: October 3, 2005, 07:44:10
Job time : 96 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2005, 07:30:50 ; Search time 90 Seconds
(without alignments)
1623.565 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
Sequence: 1 MDQVSSPIVDINYYTSEPC.....ERASSVYTRSTGEQISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1841	100.0	352	14 US-10-439-845-2	Sequence 2, Appli
2	1841	100.0	352	16 US-10-700-313-2	Sequence 2, Appli
3	1841	100.0	352	17 US-10-846-185-2	Sequence 2, Appli
4	1836	99.7	352	9 US-09-759-841-2	Sequence 15, Appli
5	1836	99.7	352	9 US-09-813-653-15	Sequence 1, Appli
6	1836	99.7	352	9 US-09-796-202-1	Sequence 5, Appli
7	1836	99.7	352	9 US-09-938-719-5	Sequence 5, Appli
8	1836	99.7	352	9 US-09-939-226-5	Sequence 5, Appli
9	1836	99.7	352	9 US-09-938-703-5	Sequence 14, Appli
10	1836	99.7	352	10 US-09-734-221A-14	Sequence 2, Appli
11	1836	99.7	352	13 US-10-106-623-2	

12	1836	99.7	352	14 US-10-086-814-1	Sequence 1, Appli
13	1836	99.7	352	14 US-10-290-058A-6	Sequence 6, Appli
14	1836	99.7	352	14 US-10-225-567A-352	Sequence 352, App
15	1836	99.7	352	14 US-10-323-314-1	Sequence 1, Appli
16	1836	99.7	352	14 US-10-072-301-1	Sequence 1, Appli
17	1836	99.7	352	14 US-10-071-866-1	Sequence 1, Appli
18	1836	99.7	352	14 US-10-239-423-67	Sequence 67, Appli
19	1836	99.7	352	14 US-10-439-845-4	Sequence 4, Appli
20	1836	99.7	352	15 US-10-360-828-1	Sequence 1, Appli
21	1836	99.7	352	16 US-10-661-798-5	Sequence 5, Appli
22	1836	99.7	352	16 US-10-612-791-5	Sequence 5, Appli
23	1836	99.7	352	16 US-10-772-037-2	Sequence 2, Appli
24	1836	99.7	352	16 US-10-723-860-4095	Sequence 4095, Ap
25	1836	99.7	352	16 US-10-700-313-4	Sequence 4, Appli
26	1836	99.7	352	17 US-10-486-471-10	Sequence 10, Appli
27	1836	99.7	352	17 US-10-846-185-4	Sequence 4, Appli
28	1836	99.7	352	18 US-10-988-485-1	Sequence 1, Appli
29	1836	99.7	352	18 US-10-756-143-5721	Sequence 5721, Ap
30	1836	99.7	352	18 US-10-287-436A-432	Sequence 432, App
31	1836	99.7	352	18 US-10-287-436A-1133	Sequence 1133, Ap
32	1830	99.4	352	9 US-09-813-653-17	Sequence 17, Appli
33	1830	99.4	352	10 US-09-826-509-477	Sequence 477, App
34	1830	99.4	352	14 US-10-164-649-52	Sequence 52, Appli
35	1830	99.4	352	17 US-10-925-095-477	Sequence 477, App
36	1828	99.3	352	9 US-09-725-285-2	Sequence 2, Appli
37	1828	99.3	352	9 US-09-779-879A-22	Sequence 22, Appli
38	1828	99.3	352	9 US-09-779-880A-22	Sequence 22, Appli
39	1828	99.3	352	9 US-09-195-662A-2	Sequence 2, Appli
40	1828	99.3	352	9 US-09-339-912A-2	Sequence 2, Appli
41	1828	99.3	352	9 US-09-502-783A-2	Sequence 2, Appli
42	1828	99.3	352	14 US-10-232-686-2	Sequence 2, Appli
43	1828	99.3	352	14 US-10-067-800-22	Sequence 22, Appli
44	1828	99.3	352	14 US-10-135-839-22	Sequence 22, Appli
45	1828	99.3	352	16 US-10-791-905-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-439-845-2
; Sequence 2, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; AND THERAPEUTIC AGENTS FOR HIV INFECTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-2

Query Match 100.0%; Score 1841; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60

QY 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
DB 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120

QY 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
DB 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180

QY 181 HPFYSQYQFKNFQTLKIVILGLVPLLVWVICYSGLKTLRLCRNEKRRHRAVRLIFTI 240
DB 181 HPFYSQYQFKNFQTLKIVILGLVPLLVWVICYSGLKTLRLCRNEKRRHRAVRLIFTI 240

QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 2
US-10-700-313-2
; Sequence 2, Application US/10700313
; Publication No. US20040259785A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10700,313
; FILING DATE: 31-Oct-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-700-313-2

Query Match 100.0%; Score 1841; DB 16; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILINCKR 60

QY 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
DB 61 LKSMTDIYLLNLAIASDLFELLTPFWAHYLAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120

QY 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
DB 121 LLTDIYLAHVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180

QY 181 HPFYSQYQFKNFQTLKIVILGLVPLLVWVICYSGLKTLRLCRNEKRRHRAVRLIFTI 240
DB 181 HPFYSQYQFKNFQTLKIVILGLVPLLVWVICYSGLKTLRLCRNEKRRHRAVRLIFTI 240

QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 3
US-10-846-185-2
; Sequence 2, Application US/10846185
; Publication No. US20050118677A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/846,185
; FILING DATE: 14-May-2004
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-846-185-2

Query Match 100.0%; Score 1841; DB 17; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.9e-143;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
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DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
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DB 181 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
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DB 241 MIYVFLFWAPYNIYLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNVLVFPFKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNVLVFPFKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 4

US-09-759-841-2
Sequence 2, Application US/09759841
Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Perros, Mancoscos
TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000659.3
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 121 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 121 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 181 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 181 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 241 MIYVFLFWAPYNIYLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYNIYLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNVLVFPFKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNVLVFPFKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 5

US-09-813-653-15
Sequence 15, Application US/09813653
Patent No. US20020064770A1
GENERAL INFORMATION:
APPLICANT: Nestor, John
APPLICANT: Wilson, Carol
APPLICANT: See, Raymond
APPLICANT: Tan Hehr, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
TYPE: PRT
LENGTH: 352
ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFFGVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 121 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 121 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 181 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
DB 181 LKSMTDIYLLNLALISDLFFLLTVFPFWAHYLAQWDFGNTWCQLLTGLYFTGFSGIFPII 120
QY 241 MIYVFLFWAPYNIYLLNTFQEFGLNCSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352

RESULT 6
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCOQLLTGLYFIQFGSGIFFII 120
Db 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCOQLLTGLYFIQFGSGIFFII 120
QY 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITVWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITVWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPYISOYQPKNFQTLKIVILGLVPLVWVICYSGLIKTLARCNEKKRHRVRLIFTI 240
Db 181 HPYISOYQPKNFQTLKIVILGLVPLVWVICYSGLIKTLARCNEKKRHRVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352

RESULT 7
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/938,719
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCOQLLTGLYFIQFGSGIFFII 120
Db 61 LKSMTDIYLLNLAIISDLFLLTVPFWAHYLAQWDFGNTMCOQLLTGLYFIQFGSGIFFII 120
QY 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITVWVAVFASLPGIIFTRSQKGLHYTCSS 180
Db 121 LTIIDRYLAVHVAHFALKARTVTFGVVTSVITVWVAVFASLPGIIFTRSQKGLHYTCSS 180
QY 181 HPYISOYQPKNFQTLKIVILGLVPLVWVICYSGLIKTLARCNEKKRHRVRLIFTI 240
Db 181 HPYISOYQPKNFQTLKIVILGLVPLVWVICYSGLIKTLARCNEKKRHRVRLIFTI 240
QY 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
Db 241 MIVYFLWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKFCCKCSIFQOEAPERASSVYTRSTGGEISVGL 352

RESULT 8
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA

COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
QY 61 LKSWTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIPFII 120
DB 61 LKSWTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIPFII 120
QY 121 LLTIIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
DB 121 LLTIIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYSQYQWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYINVLNLTQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 9
US-09-938-703-5
Sequence 5, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA

COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
QY 61 LKSWTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIPFII 120
DB 61 LKSWTDIYLLNLAISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFTGFSGIPFII 120
QY 121 LLTIIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
DB 121 LLTIIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSOKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
DB 181 HPFYSQYQWKNFQTLKIVILGLVPLLVNVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLNLTQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIYVFLFWAPYINVLNLTQEFPLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 10
US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELLMETTER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

```
; ; Floor
; ; CITY: Hackensack
; ; STATE: New Jersey
; ; COUNTRY: USA
; ; ZIP: 07601
; ;
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent in Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/09/734,221A
; ; FILING DATE: 11-Dec-2000
; ; CLASSIFICATION: <Unknown>
; ;
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: US 08/666,020
; ; FILING DATE: 19-JUN-1996
; ; APPLICATION NUMBER: US 08/227,319
; ; FILING DATE: 13-APR-1994
; ;
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Jackson Esq., David A.
; ; REGISTRATION NUMBER: 26,742
; ; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 201-487-5800
; ; TELEFAX: 201-343-1684
; ;
; ; INFORMATION FOR SEQ ID NO: 14:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 352 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; HYPOTHETICAL: NO
; ; ORIGINAL SOURCE:
; ; ORGANISM: Homo sapiens
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
; ; US-09-734-221A-14
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Query Match 99.7%; Score 1836; DB 10; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIGFPGSGIFFII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIGFPGSGIFFII 120
QY 121 LTTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
DB 121 LTTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPYISOYQWKNFQTLKIVILGLVPLLVVVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HPYISOYQWKNFQTLKIVILGLVPLLVVVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
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RESULT 11

US-10-106-623-2

; Sequence 2, Application US/10106623

; Publication No. US20020150888A1

; GENERAL INFORMATION:

```
; ;
; ; APPLICANT: Gray, Patrick W.
; ; Schweickart, Vicky L.
; ; Raport, Carol J.
; ; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; ; NUMBER OF SEQUENCES: 20
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; ; CITY: Chicago
; ; STATE: Illinois
; ; COUNTRY: USA
; ; ZIP: 60606
; ;
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent in Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/10/106,623
; ; FILING DATE: 26-Mar-2002
; ; CLASSIFICATION: <Unknown>
; ; PRIOR APPLICATION DATA:
; ; APPLICATION NUMBER: 08/771,276
; ; FILING DATE: <Unknown>
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: No. US20020150888Aland, Greta E.
; ; REGISTRATION NUMBER: 35,302
; ; REFERENCE/DOCKET NUMBER: 27866/33670
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 312-474-6300
; ; TELEFAX: 312-474-0448
; ;
; ; INFORMATION FOR SEQ ID NO: 2:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 352 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; FEATURE:
; ; NAME/KEY: misc feature
; ; OTHER INFORMATION: /= "88C amino acid sequence"
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; ; US-10-106-623-2
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Query Match 99.7%; Score 1836; DB 13; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIGFPGSGIFFII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYLAQAQWDFGNTWCQLLTGLYFIGFPGSGIFFII 120
QY 121 LTTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
DB 121 LTTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSS 180
QY 181 HPYISOYQWKNFQTLKIVILGLVPLLVVVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HPYISOYQWKNFQTLKIVILGLVPLLVVVICYSIGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIIVLLNTFQEFFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRFCKCCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
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RESULT 12

US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana C.
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60

QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120

QY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

QY 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352

RESULT 13
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE REFERENCE: MP101-289PIRM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60

DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120

QY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

QY 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352

RESULT 14
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR 60

QY 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120
DB 61 LKSMTDIYLLNLALISDLFFLLTVPFWAHYLAQAQWDFGNTWCQLLTGLYFIQFSGIFPII 120

QY 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

QY 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240
DB 181 HPYISOYQFWKQFQTLKIVILGLVPLLVNVCYSGLKTLKLCRNEKKHRAVRLIFTI 240

QY 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYNIIVLLNTFQEFGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFV 300

QY 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352
DB 301 GEKFRNYLLVFFQKHAKRFCKCCSIFQEQAPERASSVYTRSTGEQEISVGL 352

Db 301 GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL 352

RESULT 15

US-10-323-314-1
 ; Sequence 1, Application US/10323314
 ; Publication No. US20030139571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dragic, Tatjana
 ; APPLICANT: Olson, William
 ; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
 ; FILE REFERENCE: 2048/61010-1/JFW/MAF/DJK
 ; CURRENT APPLICATION NUMBER: US/10/323,314
 ; CURRENT FILING DATE: 2002-12-19
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-10-323-314-1

Query Match	99.7%	Score 1836;	DB 14;	Length 352;
Best Local Similarity	99.7%	Pred. No. 1.3e-142;		
Matches 351;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	MDYQVSSPIYDINNYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR	60
Db	1	MDYQVSSPIYDINNYTSEPCKINVKQIAARLLPPLYSLVFIQFVGNMLVILILINCKR	60
QY	61	LKSMTDIYLNLAISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFGFSGIFPII	120
Db	61	LKSMTDIYLNLAISDLFLLTPFWAHYLAQWDFGNTWCQLLTGLYFIFGFSGIFPII	120
QY	121	LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS	180
Db	121	LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS	180
QY	181	HPFYSQYQFQWKNFQTLKIVILGLVPLLVNVIQYSGILKTLRCRNEKKHRAVRLIFTI	240
Db	181	HPFYSQYQFQWKNFQTLKIVILGLVPLLVNVIQYSGILKTLRCRNEKKHRAVRLIFTI	240
QY	241	MIYVFLFWAPYNIYVLLNTFQEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV	300
Db	241	MIYVFLFWAPYNIYVLLNTFQEFGLNCCSSNRLDQAMQVETLGTHTCCINPIIYAFV	300
QY	301	GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL	352
Db	301	GEKFRNYLLVFFQKHIAKRFCKCSIFQQEAPERASSVYTRSTGEQEISVGL	352

Search completed: October 3, 2005, 07:47:26
 Job time : 91 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: . October 3, 2005, 07:34:24 ; Search time 28 Seconds
(without alignments)
938.445 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYITSEPC.....ERASSVYTRSTGQEISVGL 352
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	3	US-09-087-232A-13
2	1836	99.7	352	3	US-08-861-105-14
3	1836	99.7	352	3	US-08-575-967A-2
4	1836	99.7	352	4	US-08-833-752-5
5	1836	99.7	352	4	US-09-796-202-1
6	1836	99.7	352	4	US-09-938-719-5
7	1836	99.7	352	4	US-08-771-276-2
8	1836	99.7	352	4	US-09-939-226B-5
9	1830	99.4	352	3	US-09-045-583-52
10	1830	99.4	352	3	US-09-534-185-52
11	1830	99.4	352	4	US-09-826-509-477
12	1828	99.3	352	4	US-09-502-783A-2
13	1828	99.3	352	4	US-09-502-784A-2
14	1828	99.3	352	4	US-09-339-912A-2
15	1828	99.3	352	4	US-09-195-662A-2
16	1821	98.9	352	3	US-08-466-343D-2
17	1809	98.3	352	3	US-09-517-605-5
18	1802	97.9	352	4	US-08-771-276-20
19	1541	83.7	354	3	US-08-724-984A-2
20	1360	73.9	360	4	US-09-131-827A-20
21	1359	73.8	347	1	US-08-461-244-3
22	1359	73.8	360	1	US-08-450-393A-4
23	1359	73.8	360	3	US-08-446-669-4
24	1359	73.8	360	3	US-09-045-583-50
25	1359	73.8	360	4	US-09-534-185-50
26	1359	73.8	360	4	US-09-131-827A-2
27	1359	73.8	360	4	US-09-625-573-4

28 1359 73.8 360 5 PCT-US95-00476-4 Sequence 4, Appli
29 1359 73.8 377 4 US-09-949-016-11221 Sequence 11221, A
30 1353 73.5 360 4 US-09-826-509-473 Sequence 473, App
31 1345 73.1 360 4 US-08-833-752-7 Sequence 7, Appli
32 1345 73.1 360 4 US-09-938-719-7 Sequence 7, Appli
33 1345 73.1 360 4 US-09-939-226B-7 Sequence 7, Appli
34 1340 72.8 360 3 US-09-045-583-51 Sequence 51, Appl
35 1340 72.8 360 4 US-09-534-185-51 Sequence 51, Appl
36 1219 66.2 344 3 US-08-466-343D-9 Sequence 9, Appli
37 1219 66.2 344 4 US-09-502-784A-9 Sequence 9, Appli
38 1219 66.2 374 1 US-08-450-393A-2 Sequence 2, Appli
39 1219 66.2 374 3 US-08-446-669-2 Sequence 2, Appli
40 1219 66.2 374 4 US-10-039-659A-14 Sequence 14, Appli
41 1219 66.2 374 4 US-09-625-573-2 Sequence 2, Appli
42 1219 66.2 374 5 PCT-US95-00476-2 Sequence 2, Appli
43 1219 66.2 387 4 US-09-949-016-11222 Sequence 9, Appli
44 1133.5 61.6 329 4 US-09-502-783A-9 Sequence 9, Appli
45 1133.5 61.6 329 4 US-09-339-912A-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-087-232A-13

Query Match 99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 1;
QY 1 MDYQVSSPIYDINYITSEPCQKINVKQIAARLLPPLYSLVFIFGFGVNNMLVILLINCKR 60
Db 1 MDYQVSSPIYDINYITSEPCQKINVKQIAARLLPPLYSLVFIFGFGVNNMLVILLINCKR 60

QY	61	LKSMTDIYLLNLIAISDLFLLTPFPWAHYLAQWDFGNTMCOLLTGLYFIQFFSGIIPFII	120
Db	61	LKSMTDIYLLNLIAISDLFLLTPFPWAHYLAQWDFGNTMCOLLTGLYFIQFFSGIIPFII	120
QY	121	LITIDRYLAVVHAVFALKARTVTFGVTSVITWVAVFASLPGIITFTSRQEGHLHYTCSS	180
Db	121	LITIDRYLAVVHAVFALKARTVTFGVTSVITWVAVFASLPGIITFTSRQEGHLHYTCSS	180
QY	181	HPPSYQYQWKQFQTLKIVILGLVPLIWMVICYSGILKTLILRCNEKKRRHRAVRLIFTI	240
Db	181	HPPSYQYQWKQFQTLKIVILGLVPLIWMVICYSGILKTLILRCNEKKRRHRAVRLIFTI	240
QY	241	MIYFLFWAPYINIVLLNTFQBFPGLNLCSSNRLLDQAMQVTTETLGMTHCCINPIIYAFV	300
Db	241	MIYFLFWAPYINIVLLNTFQBFPGLNLCSSNRLLDQAMQVTTETLGMTHCCINPIIYAFV	300
QY	301	GEXFRNLYLVFFOKHIAKEFCCKCSIFQOEAPERASSVYTRSTGBOEISVGL	352
Db	301	GEXFRNLYLVFFOKHIAKEFCCKCSIFQOEAPERASSVYTRSTGBOEISVGL	352

RESULT 2
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELMMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Db 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Db 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 4

US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 648375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-5

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Db 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Db 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352
Db 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 5

US-09-796-202-1
Sequence 1, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILINCKR 60
Qy 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Db 61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQWDFGNTMCQLLTGLYFIQFGSGIFFII 120
Qy 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFKARTVTGVTSTVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Db 181 HPYQYQFWKQFQTLKIVILGLVPLLVVVICYSGLIKTLRCRNEKKHRAVRLIFTI 240
Qy 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNIIVLLNTFQBFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Qy 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

Db 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 6
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. 6692938
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGPFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGPFSGIFFII 120
QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVLPVLLVMVICYSGLIKTLRLCRNEKKRHRAVRLIFTI 240
Db 181 HPFYSQYQWKNFQTLKIVILGLVLPVLLVMVICYSGLIKTLRLCRNEKKRHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLILNTFQEFPGFLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIYVFLFWAPYINVLILNTFQEFPGFLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

Db 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 7
US-08-771-276-2
; Sequence 2, Application US/08771276
; Patent No. 6797811
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 679781land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
US-08-771-276-2

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFGVGNMLVILILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGPFSGIFFII 120
Db 61 LKSMTDIYLLNLAISDLFLLTPFWAHYLAQWDFGNMTCQLLTGLYIFGPFSGIFFII 120
QY 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
Db 121 LLTIDRYLAVVHAFVAFKARTVTFGVVTSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
QY 181 HPFYSQYQWKNFQTLKIVILGLVLPVLLVMVICYSGLIKTLRLCRNEKKRHRAVRLIFTI 240
Db 181 HPFYSQYQWKNFQTLKIVILGLVLPVLLVMVICYSGLIKTLRLCRNEKKRHRAVRLIFTI 240
QY 241 MIYVFLFWAPYINVLILNTFQEFPGFLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db 241 MIYVFLFWAPYINVLILNTFQEFPGFLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
QY 301 GEFKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEISVGL 352

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 24-Mar-2000
APPLICATION NUMBER: US/09/534,185
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Query Match 99.4%; Score 1830; DB 4; Length 352;
Best Local Similarity 99.1%; Pred. No. 3.6e-146;
Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
DB 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCCQLLTGLYFIQFSGIFII 120
DB 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCCQLLTGLYFIQFSGIFII 120
QY 121 LLTIDRYLAVHVAFAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPYISQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240
DB 181 HPYISQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240
QY 241 MIVYFLFWAPYINVLNLTNFOEFFGLNCCSSNRLDQAMQVTLGTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYINVLNLTNFOEFFGLNCCSSNRLDQAMQVTLGTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 11

US-09-826-509-477
Sequence 477, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liao, Chen W.
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G Protein-Coupled Receptors

FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patent in Version 2.1
SEQ ID NO 477
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 99.4%; Score 1830; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 3.6e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
DB 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
QY 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCCQLLTGLYFIQFSGIFII 120
DB 61 LKSMTDIYLNLALISDLFFLLTPFWAHYLAQWDFGNTMCCQLLTGLYFIQFSGIFII 120
QY 121 LLTIDRYLAVHVAFAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAFKARTVTFGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HPYISQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240
DB 181 HPYISQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240
QY 241 MIVYFLFWAPYINVLNLTNFOEFFGLNCCSSNRLDQAMQVTLGTHCCINPIIYAFV 300
DB 241 MIVYFLFWAPYINVLNLTNFOEFFGLNCCSSNRLDQAMQVTLGTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 12

US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR 2)
TITLE OF INVENTION: HDGNR10
FILE REFERENCE: 1488, 1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60
DB 1 MDYQSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIQFVGNMVLVILINCKR 60

QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
DB 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352

RESULT 13

US-09-502-784A-2
; Sequence 2, Application US/09502784A
; Patent No. 6743594

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Methods of Screening Using Human G-Protein

TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)

FILE REFERENCE: 1488.1150005

CURRENT APPLICATION NUMBER: US/09/502,784A

CURRENT FILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: 09/195,662

PRIOR FILING DATE: 1998-11-18

PRIOR APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 2

LENGTH: 352

TYPE: PRT

ORGANISM: Homo sapiens

US-09-502-784A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
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DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
DB 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352

RESULT 14

US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. 6759519

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

TITLE OF INVENTION: (CCR5 Receptor)

FILE REFERENCE: 1488.1150003

CURRENT APPLICATION NUMBER: US/09/339,912A

CURRENT FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: 09/195,662

PRIOR FILING DATE: 1998-11-18

PRIOR APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 352

TYPE: PRT

ORGANISM: Artificial Sequence: Genomic

FEATURE:

OTHER INFORMATION: Deduced Amino Acid Sequence

US-09-339-912A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
DB 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVIFGFVGNMLVILINCKR 60
QY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGSGIFFII 120
QY 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
DB 121 LLTIDRYLAVHVAFAKARTVTFGVVTSVITWVAVFASLPGLIIFTRSQEGLHYTCSS 180
QY 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
DB 181 HPFYSQVQWKNFQTLKIVILGLVPLLVWVICVSGILKTLRCRNEKKEHRAVRLIFTI 240
QY 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
DB 241 MIVYFLWAPYNI VLLNTQEF FGLNCCSSNRLDQAMQVTTGLGTHCCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQQAEPERASSVYTRSTGEQISVGL 352

RESULT 15

US-09-195-662A-2

; Sequence 2, Application US/09195662A

; Patent No. 6800729

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)

FILE REFERENCE: 1488.1150002

CURRENT APPLICATION NUMBER: US/09/195,662A

CURRENT FILING DATE: 1998-11-18

PRIOR APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match      99.3%; Score 1828; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 5.3e-146;
Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVIFPGFVGNMLVILILINCKR 60
Db      1 MDYQVSSPIYDINNYTSEPCQKINVKQIAARLLPPLYSLVIFPGFVGNMLVILILINCKR 60

QY      61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120
Db      61 LKSMTDIYLLNLALISDLFFLLTPFWAHYLAQAQWDFGNTMCQLLTGLYFIFGFSGIFFTI 120

QY      121 LLTIDRYLAVVHVAFAKARTVTFGVTSVITWVAVFASLPGIIFRSQKEGLHYTCSS 180
Db      121 LLTIDRYLAVVHVAFAKARTVTFGVTSVITWVAVFASLPGIIFRSQKEGLHYTCSS 180

QY      181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240
Db      181 HFPYSQYQFWKNFQTLKIVILGLVPLLVNVCYSGILKTLRCRNEKKRHRVRLIFTI 240

QY      241 MIVYFLFWAPYNIIVLLNTFQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300
Db      241 MIVYFLFWAPYNIIVLLNTFQEPFGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFV 300

QY      301 GEKFRNYLLVFFQKHAKRCKCCSIFQQAPEPERSVYTRSTGEQEISVGL 352
Db      301 GEKFRNYLLVFFQKHAKRCKCCSIFQQAPEPERSVYTRSTGEQEISVGL 352
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Job time : 30 secs